

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:18 ; Search time 37.2991 Seconds
(without alignments)
165.965 Million cell updates/sec

Title: US-09-843-221A-170

Perfect score: 39

Sequence: 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75810

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*

10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*

12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*

16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*

19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	39	100.0	39	22	AAB80490	PTH2 receptor bind
2	39	100.0	39	23	ABB82202	TIP39 polypeptide
3	39	100.0	39	23	AAE23970	Human TIP39 mature
4	39	100.0	39	24	ABP56764	Human TIP39 protein
5	39	100.0	40	23	AAU73181	Parathyroid hormone
6	38	97.4	38	22	AAB80489	PTH2 receptor bind
7	38	97.4	38	22	AAB80526	PTH2 receptor bind
8	37	94.9	37	22	AAB80488	PTH2 receptor bind
9	37	94.9	37	22	AAB80525	PTH2 receptor bind
10	37	94.9	37	23	ABB82197	TIP39 truncated peptide
11	36	92.3	36	22	AAB80487	PTH2 receptor bind
12	36	92.3	36	22	AAB80524	PTH2 receptor bind
13	35	89.7	35	22	AAB80486	PTH2 receptor bind
14	35	89.7	35	22	AAB80523	PTH2 receptor bind
15	35	89.7	35	22	AAB80527	PTH2 receptor bind
16	34	87.2	34	22	AAB80485	PTH2 receptor bind
17	34	87.2	34	22	AAB80522	PTH2 receptor bind
18	34	87.2	34	22	AAB80528	PTH2 receptor bind
19	33	84.6	33	22	AAB80484	PTH2 receptor bind
20	33	84.6	33	22	AAB80521	PTH2 receptor bind
21	33	84.6	33	22	AAB80529	PTH2 receptor bind
22	32	82.1	32	22	AAB80483	PTH2 receptor bind
23	32	82.1	32	22	AAB80520	PTH2 receptor bind
24	32	82.1	32	22	AAB80530	PTH2 receptor bind
25	32	82.1	32	23	ABB82198	TIP39 truncated peptide
26	31	79.5	31	22	AAB80482	PTH2 receptor bind
27	31	79.5	31	22	AAB80519	PTH2 receptor bind
28	31	79.5	31	22	AAB80531	PTH2 receptor bind
29	31	79.5	31	23	ABB82196	TIP39 truncated peptide
30	30	76.9	30	22	AAB80481	PTH2 receptor bind
31	30	76.9	30	22	AAB80518	PTH2 receptor bind
32	30	76.9	30	22	AAB80532	PTH2 receptor bind
33	30	76.9	30	23	ABB82199	TIP39 truncated peptide
34	29	74.4	29	22	AAB80480	PTH2 receptor bind
35	29	74.4	29	22	AAB80517	PTH2 receptor bind
36	29	74.4	29	22	AAB80533	PTH2 receptor bind
37	29	74.4	29	23	ABB82200	TIP39 truncated peptide
38	28	71.8	28	22	AAB80479	PTH2 receptor bind
39	28	71.8	28	22	AAB80516	PTH2 receptor bind
40	28	71.8	28	22	AAB80534	PTH2 receptor bind
41	28	71.8	28	23	ABB82201	TIP39 truncated peptide
42	28	71.8	37	23	ABB82208	Chimeric PTH1R ago
43	24	61.5	37	23	ABB82209	Chimeric PTH1R ago
44	18	46.2	37	23	ABB82207	Chimeric PTH1R ago
45	6	15.4	28	20	AYY33524	Human p75NTR dependent
46	6	15.4	30	23	AAU84792	HCV HepC1a segment
47	6	15.4	30	23	AAU84793	HCV HepC1a segment
48	6	15.4	31	21	AYY77381	HIV-1 group O env
49	6	15.4	31	21	AYY77382	HIV-1 group O env
50	6	15.4	37	17	AAW07210	HIV-1 group O strain

51	6	15.4	38	21	AAB14568	HIV-1 isolate CM.A
52	6	15.4	38	22	AAU70740	HIV viral envelope
53	6	15.4	38	22	AAG63895	Amino acid sequenc
54	6	15.4	40	17	AAW07343	Partial sequence o
55	6	15.4	40	17	AAW07344	Partial sequence o
56	6	15.4	40	17	AAW07346	Partial sequence o
57	6	15.4	40	17	AAW07347	Partial sequence o
58	6	15.4	40	17	AAW07352	Partial sequence o
59	5	12.8	28	20	AAY33508	Human p75NTR deriv
60	5	12.8	28	20	AAY33509	Human p75NTR deriv
61	5	12.8	28	20	AAY33510	Human p75NTR deriv
62	5	12.8	28	20	AAY33511	Human p75NTR deriv
63	5	12.8	28	20	AAY33525	Human p75NTR depen
64	5	12.8	28	22	ABG52079	Human liver peptid
65	5	12.8	28	22	ABG52416	Human liver peptid
66	5	12.8	28	22	ABB32003	Peptide #4654 enco
67	5	12.8	28	22	ABB32347	Peptide #4998 enco
68	5	12.8	28	22	ABB37251	Peptide #4757 enco
69	5	12.8	28	22	ABB37608	Peptide #5114 enco
70	5	12.8	28	22	ABB43366	Peptide #10872 enc
71	5	12.8	28	22	ABB22547	Protein #4546 enco
72	5	12.8	28	22	ABB22899	Protein #4898 enco
73	5	12.8	28	22	AAM57958	Human brain expres
74	5	12.8	28	22	AAM58261	Human brain expres
75	5	12.8	28	22	AAM64280	Human brain expres
76	5	12.8	28	22	AAM70383	Human bone marrow
77	5	12.8	28	22	AAM70710	Human bone marrow
78	5	12.8	28	22	AAM77106	Human bone marrow
79	5	12.8	28	22	AAM18225	Peptide #4659 enco
80	5	12.8	28	22	AAM18568	Peptide #5002 enco
81	5	12.8	28	22	AAM30716	Peptide #4753 enco
82	5	12.8	28	22	AAM31026	Peptide #5063 enco
83	5	12.8	28	22	AAM05838	Peptide #4520 enco
84	5	12.8	28	22	AAM06136	Peptide #4818 enco
85	5	12.8	28	23	ABG78097	ITALY, LOR-2, STRI
86	5	12.8	28	23	ABJ01040	Human breast speci
87	5	12.8	28	23	ABG40027	Human peptide enco
88	5	12.8	28	23	ABG40434	Human peptide enco
89	5	12.8	29	19	AAW71425	Peptide having an
90	5	12.8	29	20	AAY01414	Secreted protein e
91	5	12.8	29	21	AAB08357	Amino acid sequenc
92	5	12.8	29	21	AAV95951	Synthetic coiled-c
93	5	12.8	29	21	AAV67645	Peptide #45 for de
94	5	12.8	29	21	AAV67646	Peptide #46 for de
95	5	12.8	29	21	AAV67655	Peptide #55 for de
96	5	12.8	29	21	AAV67656	Peptide #56 for de
97	5	12.8	29	21	AAV67718	Peptide #118 for d
98	5	12.8	29	21	AAV67719	Peptide #119 for d
99	5	12.8	29	21	AAV67728	Peptide #128 for d
100	5	12.8	29	21	AAV67729	Peptide #129 for d
101	5	12.8	29	22	ABG02689	Novel human diagno
102	5	12.8	29	22	AAB81490	Leucine zipper oli
103	5	12.8	30	19	AAW71426	Peptide having an
104	5	12.8	30	21	AAV67636	Peptide #36 for de
105	5	12.8	30	21	AAV67638	Peptide #38 for de
106	5	12.8	30	21	AAV67709	Peptide #109 for d
107	5	12.8	30	21	AAV67711	Peptide #111 for d

108	5	12.8	30	22	ABB50666	Human secreted pro
109	5	12.8	30	22	AAO08695	Human polypeptide
110	5	12.8	30	24	AAE30257	Human LP289 signal
111	5	12.8	31	18	AAW24743	Heel domain of OP-
112	5	12.8	31	19	AAW71427	Peptide having an
113	5	12.8	31	19	AAW80536	Peptide having bet
114	5	12.8	31	19	AAW80538	Peptide having bet
115	5	12.8	31	19	AAW80540	Peptide having bet
116	5	12.8	31	19	AAW80542	Peptide having bet
117	5	12.8	31	19	AAW80544	Peptide having bet
118	5	12.8	31	21	AAY67665	Peptide #65 for de
119	5	12.8	31	21	AAY67666	Peptide #66 for de
120	5	12.8	31	21	AAY67702	Peptide #102 for d
121	5	12.8	31	21	AAY67703	Peptide #103 for d
122	5	12.8	31	21	AAY67738	Peptide #138 for d
123	5	12.8	31	21	AAY67739	Peptide #139 for d
124	5	12.8	31	21	AAY67775	Peptide #175 for d
125	5	12.8	31	21	AAY67776	Peptide #176 for d
126	5	12.8	31	23	AAG79849	BMP-7 heel cyclic
127	5	12.8	32	18	AAW36891	Cyclised peptide H
128	5	12.8	32	19	AAW71428	Peptide having an
129	5	12.8	32	19	AAW80537	Peptide having bet
130	5	12.8	32	19	AAW71446	Peptide having an
131	5	12.8	32	19	AAW71439	Peptide having an
132	5	12.8	32	19	AAW71441	Peptide having an
133	5	12.8	32	19	AAW71444	Peptide having an
134	5	12.8	32	21	AAY67643	Peptide #43 for de
135	5	12.8	32	21	AAY67644	Peptide #44 for de
136	5	12.8	32	21	AAY67653	Peptide #53 for de
137	5	12.8	32	21	AAY67654	Peptide #54 for de
138	5	12.8	32	21	AAY67716	Peptide #116 for d
139	5	12.8	32	21	AAY67717	Peptide #117 for d
140	5	12.8	32	21	AAY67727	Peptide #127 for d
141	5	12.8	32	22	AAU11255	Human osteogenic p
142	5	12.8	32	23	AAG79853	BMP-7 based peptid
143	5	12.8	32	23	ABB76453	BMP-7 antagonist h
144	5	12.8	32	23	ABB76283	Mature human osteo
145	5	12.8	32	24	AAE30262	Human LP319a prote
146	5	12.8	32	24	AAE30266	Human LP319b prote
147	5	12.8	33	11	AAR05848	Reagent of GTP-bin
148	5	12.8	33	11	AAR09313	Reagent of GTP-bin
149	5	12.8	33	19	AAW71421	Peptide having an
150	5	12.8	33	19	AAW71429	Peptide having an
151	5	12.8	33	19	AAW80547	Peptide having bet
152	5	12.8	33	19	AAW71447	Peptide having an
153	5	12.8	33	19	AAW71450	Peptide having an
154	5	12.8	33	19	AAW71451	Peptide having an
155	5	12.8	33	19	AAW71440	Peptide having an
156	5	12.8	33	19	AAW71443	Peptide having an
157	5	12.8	33	19	AAW71445	Peptide having an
158	5	12.8	33	21	AAY67635	Peptide #35 for de
159	5	12.8	33	21	AAY67637	Peptide #37 for de
160	5	12.8	33	21	AAY67708	Peptide #108 for d
161	5	12.8	33	21	AAY67710	Peptide #110 for d
162	5	12.8	33	22	ABG47640	Human liver peptid
163	5	12.8	33	22	ABB27618	Human peptide #269
164	5	12.8	33	22	ABB32788	Peptide #294 encod

165	5	12.8	33	22	ABB18271	Protein #270 encod
166	5	12.8	33	22	AAM53595	Human brain expres
167	5	12.8	33	22	AAM65975	Human bone marrow
168	5	12.8	33	22	AAM13843	Peptide #277 encod
169	5	12.8	33	22	AAM26250	Peptide #287 encod
170	5	12.8	33	22	AAM01587	Peptide #269 encod
171	5	12.8	33	23	ABG35622	Human peptide enco
172	5	12.8	33	23	ABB76289	Mature human osteo
173	5	12.8	33	24	AAE29925	Human LP289 splice
174	5	12.8	34	19	AAW71422	Peptide having an
175	5	12.8	34	19	AAW71430	Peptide having an
176	5	12.8	34	19	AAW71442	Peptide having an
177	5	12.8	34	19	AAW53038	HIV-1 polypeptide.
178	5	12.8	34	21	AAY67663	Peptide #63 for de
179	5	12.8	34	21	AAY67664	Peptide #64 for de
180	5	12.8	34	21	AAY67700	Peptide #100 for d
181	5	12.8	34	21	AAY67701	Peptide #101 for d
182	5	12.8	34	21	AAY67736	Peptide #136 for d
183	5	12.8	34	21	AAY67737	Peptide #137 for d
184	5	12.8	34	21	AAY67773	Peptide #173 for d
185	5	12.8	34	21	AAY67774	Peptide #174 for d
186	5	12.8	34	21	AAY64930	Human 5' EST relat
187	5	12.8	34	24	ABU70888	Human adipocyte Se
188	5	12.8	35	19	AAW71452	Peptide having an
189	5	12.8	35	19	AAW71453	Peptide having an
190	5	12.8	35	19	AAW71431	Peptide having an
191	5	12.8	35	21	AAB63179	Human secreted pro
192	5	12.8	35	21	AAB29884	Human secreted pro
193	5	12.8	35	21	AAY68726	Amino acid sequenc
194	5	12.8	35	23	ABP42061	Human ovarian anti
195	5	12.8	36	19	AAW71432	Peptide having an
196	5	12.8	36	19	AAW71435	Peptide having an
197	5	12.8	36	19	AAW71436	Peptide having an
198	5	12.8	36	20	AAY30516	Allelic peptide fo
199	5	12.8	36	21	AAY79771	HIV detection rela
200	5	12.8	36	21	AAY55785	HIV (subtype D) pe
201	5	12.8	36	22	AAB62584	Peptide antigen cr
202	5	12.8	36	22	AAB62588	Peptide antigen cr
203	5	12.8	37	19	AAW71433	Peptide having an
204	5	12.8	37	22	ABG49022	Human liver peptid
205	5	12.8	37	22	ABG28237	Novel human diagno
206	5	12.8	37	22	ABB29019	Peptide #1670 enco
207	5	12.8	37	22	ABB34184	Peptide #1690 enco
208	5	12.8	37	22	AAU69966	Human tumour rejec
209	5	12.8	37	22	ABB17893	Human nervous syst
210	5	12.8	37	22	ABB19626	Protein #1625 enco
211	5	12.8	37	22	AAM54977	Human brain expres
212	5	12.8	37	22	AAM67360	Human bone marrow
213	5	12.8	37	22	AAM15192	Peptide #1626 enco
214	5	12.8	37	22	AAM27650	Peptide #1687 enco
215	5	12.8	37	22	AAM02931	Peptide #1613 enco
216	5	12.8	37	23	ABG36993	Human peptide enco
217	5	12.8	37	24	ABP80674	N. gonorrhoeae ami
218	5	12.8	38	19	AAW71434	Peptide having an
219	5	12.8	38	23	ABB82354	Pufferfish urocort
220	5	12.8	39	20	AAY12400	Human 5' EST secre
221	5	12.8	39	22	ABG56473	Human liver peptid

222	5	12.8	39	22	ABB41032	Peptide #8538 enco
223	5	12.8	39	22	AAM61887	Human brain expres
224	5	12.8	39	22	AAM74689	Human bone marrow
225	5	12.8	39	22	AAM34805	Peptide #8842 enco
226	5	12.8	39	23	ABJ10284	Human lung specifi
227	5	12.8	39	23	ABG44502	Human peptide enco
228	5	12.8	40	20	AAY11858	Human 5' EST secre
229	5	12.8	40	22	AAO11965	Human polypeptide
230	5	12.8	40	22	AAB45730	Human 7TM clone H7
231	4	10.3	28	9	AAP80199	Sequence of vasoac
232	4	10.3	28	12	AAR10938	N-terminal sequenc
233	4	10.3	28	12	AAR11313	N-terminal of deac
234	4	10.3	28	12	AAR14755	Modified expressio
235	4	10.3	28	13	AAR27568	Pel B leader plus
236	4	10.3	28	13	AAR27570	Pel B leader to fu
237	4	10.3	28	14	AAR54342	RAE 22.E. Ambrosi
238	4	10.3	28	14	AAR54407	AMB 1-6.1. Ambros
239	4	10.3	28	14	AAR40315	VIP analogue (37).
240	4	10.3	28	15	AAR53100	Bronchodilator pep
241	4	10.3	28	15	AAR53102	Bronchodilator pep
242	4	10.3	28	15	AAR53106	Bronchodilator pep
243	4	10.3	28	16	AAR85555	Deamidating antibo
244	4	10.3	28	16	AAR72982	Calmodulin-binding
245	4	10.3	28	16	AAR64328	HSV L/ST ORF2. He
246	4	10.3	28	16	AAR70261	Partial IGF-I fusi
247	4	10.3	28	17	AAW16418	Human growth facto
248	4	10.3	28	17	AAW16419	Human growth facto
249	4	10.3	28	17	AAW16425	Human growth facto
250	4	10.3	28	17	AAW16441	Human growth facto
251	4	10.3	28	17	AAW02429	RAE 22.E comprisin
252	4	10.3	28	17	AAW02393	AMB 1-6.1 comprisi
253	4	10.3	28	19	AAV21363	Human HUPF-I mutan
254	4	10.3	28	19	AAV21018	Human glial fibril
255	4	10.3	28	19	AAW74926	Human secreted pro
256	4	10.3	28	19	AAW39968	Peptide effecting
257	4	10.3	28	19	AAW39979	Peptide effecting
258	4	10.3	28	20	AAV33513	Human p75NTR depen
259	4	10.3	28	20	AAV39255	G-protein coupled
260	4	10.3	28	20	AAV30517	Allelic peptide fo
261	4	10.3	28	20	AAV40049	Peptide sequence d
262	4	10.3	28	20	AAV40084	Peptide sequence d
263	4	10.3	28	20	AAV36409	Fragment of human
264	4	10.3	28	20	AAV07850	Human secreted pro
265	4	10.3	28	20	AAW81051	Signal peptide-cyt
266	4	10.3	28	20	AAW52786	Human growth hormo
267	4	10.3	28	20	AAW52770	Human growth hormo
268	4	10.3	28	20	AAW52763	Human growth hormo
269	4	10.3	28	20	AAW52764	Human growth hormo
270	4	10.3	28	21	AAB29919	Human secreted pro
271	4	10.3	28	21	AAB29920	Human secreted pro
272	4	10.3	28	21	AAB22003	Human V gene Vbeta
273	4	10.3	28	21	AAV71038	Streptococcus pyog
274	4	10.3	28	21	AAV95080	Leader sequence us
275	4	10.3	28	21	AAV98189	Leader sequence us
276	4	10.3	28	21	AAV79772	HIV detection rela
277	4	10.3	28	21	AAV79811	HIV infection dete
278	4	10.3	28	21	AAV51395	Human VDCCalpha1 p

279	4	10.3	28	21	AAY54385	Amino acid sequenc
280	4	10.3	28	21	AAY54393	Amino acid sequenc
281	4	10.3	28	21	AAY54401	Amino acid sequenc
282	4	10.3	28	22	ABG47988	Human liver peptid
283	4	10.3	28	22	ABG52148	Human liver peptid
284	4	10.3	28	22	ABG54715	Human liver peptid
285	4	10.3	28	22	ABG56266	Human liver peptid
286	4	10.3	28	22	ABG58974	Human liver peptid
287	4	10.3	28	22	ABG03282	Novel human diagno
288	4	10.3	28	22	ABB27966	Human peptide #617
289	4	10.3	28	22	ABB32080	Peptide #4731 enco
290	4	10.3	28	22	ABB33138	Peptide #644 encod
291	4	10.3	28	22	ABB37334	Peptide #4840 enco
292	4	10.3	28	22	ABB39655	Peptide #7161 enco
293	4	10.3	28	22	ABB40823	Peptide #8329 enco
294	4	10.3	28	22	ABB43598	Peptide #11104 enc
295	4	10.3	28	22	ABB18603	Protein #602 encod
296	4	10.3	28	22	ABB22621	Protein #4620 enco
297	4	10.3	28	22	ABB24331	Protein #6330 enco
298	4	10.3	28	22	ABB25002	Protein #7001 enco
299	4	10.3	28	22	ABB26552	Protein #8551 enco
300	4	10.3	28	22	AAM53934	Human brain expres
301	4	10.3	28	22	AAM58025	Human brain expres
302	4	10.3	28	22	AAM60367	Human brain expres
303	4	10.3	28	22	AAM61681	Human brain expres
304	4	10.3	28	22	AAM64537	Human brain expres
305	4	10.3	28	22	AAM66322	Human bone marrow
306	4	10.3	28	22	AAM70462	Human bone marrow
307	4	10.3	28	22	AAM73004	Human bone marrow
308	4	10.3	28	22	AAM74474	Human bone marrow
309	4	10.3	28	22	AAM77342	Human bone marrow
310	4	10.3	28	22	AAM89401	Human immune/haema
311	4	10.3	28	22	AAM14191	Peptide #625 encod
312	4	10.3	28	22	AAM18298	Peptide #4732 enco
313	4	10.3	28	22	AAM19801	Peptide #6235 enco
314	4	10.3	28	22	AAM20325	Peptide #6759 enco
315	4	10.3	28	22	AAM21265	Peptide #7699 enco
316	4	10.3	28	22	AAM26601	Peptide #638 encod
317	4	10.3	28	22	AAM30784	Peptide #4821 enco
318	4	10.3	28	22	AAM33228	Peptide #7265 enco
319	4	10.3	28	22	AAM34589	Peptide #8626 enco
320	4	10.3	28	22	AAM37492	Peptide #11529 enc
321	4	10.3	28	22	AAM01927	Peptide #609 encod
322	4	10.3	28	22	AAM05907	Peptide #4589 enco
323	4	10.3	28	22	AAB62595	Peptide antigen cr
324	4	10.3	28	22	AAE01634	Human gene 5 encod
325	4	10.3	28	22	AAB74345	Peptide SAF-p2A.
326	4	10.3	28	22	AAB74346	Peptide SAF-p2B.
327	4	10.3	28	22	AAB74347	Peptide SAF-p2C.
328	4	10.3	28	22	AAB74348	Peptide SAF-p2D.
329	4	10.3	28	22	AAB74349	Peptide SAF-p2E.
330	4	10.3	28	22	AAB74352	Peptide SAF-p2. U
331	4	10.3	28	22	AAB74356	Peptide used to fo
332	4	10.3	28	22	AAB68568	Peptide #2. Unide
333	4	10.3	28	22	AAB50218	Membrane disruptiv
334	4	10.3	28	22	AAB50230	Membrane disruptiv
335	4	10.3	28	23	ABG95380	Human novel secret

336	4	10.3	28	23	ABG93993	Human vasoactive i
337	4	10.3	28	23	ABG94089	Human vasoactive i
338	4	10.3	28	23	ABG78098	ITALY, LOR-2, STRI
339	4	10.3	28	23	AAE25431	Human Nod2 protein
340	4	10.3	28	23	ABJ04750	Nod2 leucine-rich
341	4	10.3	28	23	ABJ04781	Nod2 exon 11 pepti
342	4	10.3	28	23	AAO22121	Human CARD related
343	4	10.3	28	23	AAE23916	Human TCR Vbeta1 p
344	4	10.3	28	23	ABG35970	Human peptide enco
345	4	10.3	28	23	ABG40100	Human peptide enco
346	4	10.3	28	23	ABG42843	Human peptide enco
347	4	10.3	28	23	ABG44356	Human peptide enco
348	4	10.3	28	23	ABG46357	Human peptide enco
349	4	10.3	28	23	AAU91197	Human E1-E2 ATPase
350	4	10.3	28	23	AAU83142	Novel secreted pro
351	4	10.3	28	23	ABB04529	Hepatitis C capsid
352	4	10.3	28	23	ABB04559	Hepatitis C capsid
353	4	10.3	28	24	ABU56283	Human CARD-4L, Leu
354	4	10.3	28	24	ABP57664	Human CNI-00713 OR
355	4	10.3	29	8	AAP71212	Sequence of peptid
356	4	10.3	29	8	AAP71213	Sequence of peptid
357	4	10.3	29	8	AAP71214	Sequence of peptid
358	4	10.3	29	8	AAP71215	Sequence of peptid
359	4	10.3	29	8	AAP71216	Sequence of peptid
360	4	10.3	29	8	AAP71217	Sequence of peptid
361	4	10.3	29	8	AAP71218	Sequence of peptid
362	4	10.3	29	13	AAR28772	GHRF analogue pept
363	4	10.3	29	14	AAR44425	Mutant alpha-amyla
364	4	10.3	29	14	AAR44426	Mutant alpha-amyla
365	4	10.3	29	14	AAR44427	Mutant alpha-amyla
366	4	10.3	29	14	AAR44428	Mutant alpha-amyla
367	4	10.3	29	16	AAR74847	CDR3 sequence of T
368	4	10.3	29	16	AAR74848	CDR3 sequence of T
369	4	10.3	29	16	AAR74834	CDR3 sequence of T
370	4	10.3	29	17	AAW07235	HIV-1 group O stra
371	4	10.3	29	17	AAR92880	Mycobacterium 45 k
372	4	10.3	29	17	AAR89960	Synthetic human er
373	4	10.3	29	17	AAR93929	Integrin subunit b
374	4	10.3	29	18	AAW33829	CDR3 sequence of T
375	4	10.3	29	18	AAW33842	CDR3 sequence of T
376	4	10.3	29	18	AAW33843	CDR3 sequence of T
377	4	10.3	29	19	AAW75582	M. tuberculosis 45
378	4	10.3	29	19	AAW40023	Peptide effecting
379	4	10.3	29	20	AYY11909	Human 5' EST secre
380	4	10.3	29	20	AYY10849	Amino acid sequenc
381	4	10.3	29	21	AAB39209	Human secreted pro
382	4	10.3	29	21	AAB40181	Human secreted pro
383	4	10.3	29	21	AAB15448	TCR beta V-N-J reg
384	4	10.3	29	21	AAB12060	Ad7 cr1 peptide.
385	4	10.3	29	21	AAB12062	EA7 cr1 peptide.
386	4	10.3	29	21	AAB22011	Human V gene Vbeta
387	4	10.3	29	21	AYY70894	N-terminal portion
388	4	10.3	29	21	AYY70917	N-terminal portion
389	4	10.3	29	21	AYY53253	Human type enzyme
390	4	10.3	29	21	AYY79831	HIV infection dete
391	4	10.3	29	21	AYY86444	Human gene 42-enco
392	4	10.3	29	21	AYY54386	Amino acid sequenc

393	4	10.3	29	21	AAY54394	Amino acid sequenc
394	4	10.3	29	21	AAY54402	Amino acid sequenc
395	4	10.3	29	21	AAY67657	Peptide #57 for de
396	4	10.3	29	21	AAY67658	Peptide #58 for de
397	4	10.3	29	21	AAY67659	Peptide #59 for de
398	4	10.3	29	21	AAY67660	Peptide #60 for de
399	4	10.3	29	21	AAY67730	Peptide #130 for d
400	4	10.3	29	21	AAY67731	Peptide #131 for d
401	4	10.3	29	21	AAY67732	Peptide #132 for d
402	4	10.3	29	21	AAY67733	Peptide #133 for d
403	4	10.3	29	22	ABG53190	Human liver peptid
404	4	10.3	29	22	ABG54049	Human liver peptid
405	4	10.3	29	22	ABG55455	Human liver peptid
406	4	10.3	29	22	ABG55564	Human liver peptid
407	4	10.3	29	22	ABG55595	Human liver peptid
408	4	10.3	29	22	ABG57326	Human liver peptid
409	4	10.3	29	22	ABG00774	Novel human diagno
410	4	10.3	29	22	ABB38357	Peptide #5863 enco
411	4	10.3	29	22	ABB39125	Peptide #6631 enco
412	4	10.3	29	22	ABB40308	Peptide #7814 enco
413	4	10.3	29	22	ABB40334	Peptide #7840 enco
414	4	10.3	29	22	ABB41890	Peptide #9396 enco
415	4	10.3	29	22	ABB23534	Protein #5533 enco
416	4	10.3	29	22	ABB24022	Protein #6021 enco
417	4	10.3	29	22	ABB24711	Protein #6710 enco
418	4	10.3	29	22	AAM58968	Human brain expres
419	4	10.3	29	22	AAM59778	Human brain expres
420	4	10.3	29	22	AAM61106	Human brain expres
421	4	10.3	29	22	AAM61135	Human brain expres
422	4	10.3	29	22	AAM62766	Human brain expres
423	4	10.3	29	22	AAM71495	Human bone marrow
424	4	10.3	29	22	AAM72362	Human bone marrow
425	4	10.3	29	22	AAM73715	Human bone marrow
426	4	10.3	29	22	AAM73814	Human bone marrow
427	4	10.3	29	22	AAM73845	Human bone marrow
428	4	10.3	29	22	AAM75584	Human bone marrow
429	4	10.3	29	22	AAM19148	Peptide #5582 enco
430	4	10.3	29	22	AAM19557	Peptide #5991 enco
431	4	10.3	29	22	AAM20110	Peptide #6544 enco
432	4	10.3	29	22	AAM31796	Peptide #5833 enco
433	4	10.3	29	22	AAM32618	Peptide #6655 enco
434	4	10.3	29	22	AAM33901	Peptide #7938 enco
435	4	10.3	29	22	AAM34000	Peptide #8037 enco
436	4	10.3	29	22	AAM34030	Peptide #8067 enco
437	4	10.3	29	22	AAM35689	Peptide #9726 enco
438	4	10.3	29	22	AAG76872	Human colon cancer
439	4	10.3	29	22	AAE03839	Human gene 22 enco
440	4	10.3	29	22	AAE03869	Human gene 22 enco
441	4	10.3	29	22	AAB62697	ABC1 protein exter
442	4	10.3	29	22	AAB81491	Leucine zipper oli
443	4	10.3	29	23	ABG95603	Human novel secret
444	4	10.3	29	23	AAE26389	Human GPR10 protei
445	4	10.3	29	23	ABP62086	Human secreted pro
446	4	10.3	29	23	AAU99914	Human 47476 EF-han
447	4	10.3	29	23	ABG67083	Streptavidin-bindin
448	4	10.3	29	23	AAE23924	Human TCR Vbeta7 p
449	4	10.3	29	23	ABG64549	Human albumin fusi

450	4	10.3	29	23	ABG64550	Human albumin fusi
451	4	10.3	29	23	ABG41308	Human peptide enco
452	4	10.3	29	23	ABG42178	Human peptide enco
453	4	10.3	29	23	ABG43592	Human peptide enco
454	4	10.3	29	23	ABG43703	Human peptide enco
455	4	10.3	29	23	AAU91212	Human E1-E2 ATPase
456	4	10.3	29	23	AAE16229	Human betaig-h3 fi
457	4	10.3	29	23	ABB04551	Hepatitis C capsid
458	4	10.3	29	24	ABG74421	M. tuberculosis ex
459	4	10.3	29	24	ABU57605	Synthetic peptide
460	4	10.3	29	24	ABP60610	Rat insulin recept
461	4	10.3	29	24	ABJ18866	Human Bcl-XL-bindi
462	4	10.3	29	24	ABJ18879	Human Bcl-XL-bindi
463	4	10.3	30	2	AAP10040	Sequence encoded b
464	4	10.3	30	4	AAP30309	Sequence of peptid
465	4	10.3	30	9	AAP82087	Polypeptide pN4(30
466	4	10.3	30	9	AAP81553	Human insulin acce
467	4	10.3	30	10	AAP90125	Pectate lyase sign
468	4	10.3	30	13	AAR24421	Sequence of T help
469	4	10.3	30	13	AAR25214	Immunosuppressive
470	4	10.3	30	15	AAR47980	L. brevis DSM20556
471	4	10.3	30	15	AAR37123	Decarbamylase N-te
472	4	10.3	30	16	AAR74833	CDR3 sequence of T
473	4	10.3	30	16	AAR78750	PelB leader peptid
474	4	10.3	30	16	AAR75651	Human placenta der
475	4	10.3	30	16	AAR85676	45 kD M.tuberculos
476	4	10.3	30	17	AAR89965	Synthetic human er
477	4	10.3	30	18	AAW34148	Analogue #4 of HTL
478	4	10.3	30	18	AAW33828	CDR3 sequence of T
479	4	10.3	30	18	AAW22398	Human urocortin pe
480	4	10.3	30	18	AAW16345	Erwinia carotovora
481	4	10.3	30	18	AAW14016	N-terminus of Stap
482	4	10.3	30	18	AAW10244	Pel B signal seque
483	4	10.3	30	18	AAW18194	N-terminal sequenc
484	4	10.3	30	19	AAW74852	Human secreted pro
485	4	10.3	30	19	AAW47516	Erwinia carotovora
486	4	10.3	30	19	AAW47523	Erwinia carotovora
487	4	10.3	30	19	AAW41075	Erwinia carotovora
488	4	10.3	30	20	AYY33140	Rabbit liver carbo
489	4	10.3	30	20	AYY17970	Peptide Seq ID No:
490	4	10.3	30	20	AYY13409	Peptide from HSV1
491	4	10.3	30	20	AYY07214	Peptide transfecti
492	4	10.3	30	20	AAW89542	A pectate lyase pe
493	4	10.3	30	21	AAB62906	Human MGST-II alte
494	4	10.3	30	21	AAB36465	Human plakophilin
495	4	10.3	30	21	AAB34508	Human secreted pro
496	4	10.3	30	21	AAB39081	Human secreted pro
497	4	10.3	30	21	AAB45036	Human secreted pro
498	4	10.3	30	21	AAB15438	TCR beta V-N-J reg
499	4	10.3	30	21	AAB15481	TCR beta V-N-J reg
500	4	10.3	30	21	AAG35977	Arabidopsis thalia
501	4	10.3	30	21	AYY85074	Immunogenic peptid
502	4	10.3	30	21	AYY79837	HIV infection dete
503	4	10.3	30	21	AYY54387	Amino acid sequenc
504	4	10.3	30	21	AYY54395	Amino acid sequenc
505	4	10.3	30	21	AYY54403	Amino acid sequenc
506	4	10.3	30	21	AYY67639	Peptide #39 for de

507	4	10.3	30	21	AAY67640	Peptide #40 for de
508	4	10.3	30	21	AAY67641	Peptide #41 for de
509	4	10.3	30	21	AAY67642	Peptide #42 for de
510	4	10.3	30	21	AAY67647	Peptide #47 for de
511	4	10.3	30	21	AAY67648	Peptide #48 for de
512	4	10.3	30	21	AAY67649	Peptide #49 for de
513	4	10.3	30	21	AAY67650	Peptide #50 for de
514	4	10.3	30	21	AAY67713	Peptide #113 for d
515	4	10.3	30	21	AAY67714	Peptide #114 for d
516	4	10.3	30	21	AAY67715	Peptide #115 for d
517	4	10.3	30	21	AAY67720	Peptide #120 for d
518	4	10.3	30	21	AAY67721	Peptide #121 for d
519	4	10.3	30	21	AAY67722	Peptide #122 for d
520	4	10.3	30	21	AAY67723	Peptide #123 for d
521	4	10.3	30	21	AAY67726	Peptide #126 for d
522	4	10.3	30	22	ABG53218	Human liver peptid
523	4	10.3	30	22	ABG57529	Human liver peptid
524	4	10.3	30	22	ABG00496	Novel human diagno
525	4	10.3	30	22	ABG02839	Novel human diagno
526	4	10.3	30	22	ABG07265	Novel human diagno
527	4	10.3	30	22	ABG11764	Novel human diagno
528	4	10.3	30	22	ABB38389	Peptide #5895 enco
529	4	10.3	30	22	ABB42098	Peptide #9604 enco
530	4	10.3	30	22	ABB23567	Protein #5566 enco
531	4	10.3	30	22	AAM58998	Human brain expres
532	4	10.3	30	22	AAM62978	Human brain expres
533	4	10.3	30	22	AAM71526	Human bone marrow
534	4	10.3	30	22	AAM75791	Human bone marrow
535	4	10.3	30	22	AAM88420	Human immune/haema
536	4	10.3	30	22	AAM19180	Peptide #5614 enco
537	4	10.3	30	22	AAM31826	Peptide #5863 enco
538	4	10.3	30	22	AAM35901	Peptide #9938 enco
539	4	10.3	30	22	AAB98097	Erwinia caratovora
540	4	10.3	30	22	AAB92014	Galanin peptide SE
541	4	10.3	30	23	ABP68891	Marine snail beta-
542	4	10.3	30	23	ABG95303	Human novel secret
543	4	10.3	30	23	AAU97984	Synthetic erythrop
544	4	10.3	30	23	AAU97991	Synthetic erythrop
545	4	10.3	30	23	AAU97995	Synthetic erythrop
546	4	10.3	30	23	ABG41339	Human peptide enco
547	4	10.3	30	23	ABP41453	Human ovarian anti
548	4	10.3	30	23	AAO17273	A thaliana recepto
549	4	10.3	30	23	AAU84532	HIV VPU segment 3.
550	4	10.3	30	23	AAU84533	HIV VPU segment 4.
551	4	10.3	30	23	AAU84617	HCV HepC1a segment
552	4	10.3	30	23	AAU84647	HCV HepC1a segment
553	4	10.3	30	23	AAU84665	HCV HepC1a segment
554	4	10.3	30	23	AAU84666	HCV HepC1a segment
555	4	10.3	30	23	AAU84708	HCV HepC1a segment
556	4	10.3	30	23	AAU84709	HCV HepC1a segment
557	4	10.3	30	23	AAU84797	HCV HepC1a segment
558	4	10.3	30	23	AAU84860	Human gp100 segmen
559	4	10.3	30	23	AAU84861	Human gp100 segmen
560	4	10.3	30	23	AAU84997	Human MUC1R segmen
561	4	10.3	30	23	AAU85000	Human MUC1R segmen
562	4	10.3	30	23	AAU85001	Human MUC1R segmen
563	4	10.3	30	23	AAU85067	Human PRAME segmen

564	4	10.3	30	24	ABP59412	Self-assembling tr
565	4	10.3	30	24	ABP59413	Self-assembling tr
566	4	10.3	30	24	ABR01204	Human gene 258-enc
567	4	10.3	30	24	ABU56346	M. tuberculosis ex
568	4	10.3	30	24	ABJ19714	Human secreted pro
569	4	10.3	30	24	ABP99721	Human secreted pro
570	4	10.3	30	24	ABR00921	Bioactive syntheti
571	4	10.3	30	24	ABP55255	Human histamine H2
572	4	10.3	31	8	AAP70904	Herpes simplex vir
573	4	10.3	31	11	AAR07739	Lytic peptide with
574	4	10.3	31	14	AAR42700	p19 of nef peptide
575	4	10.3	31	15	AAR54745	pRAS117 sequence b
576	4	10.3	31	16	AAR74849	CDR3 sequence of T
577	4	10.3	31	16	AAR74850	CDR3 sequence of T
578	4	10.3	31	16	AAR74851	CDR3 sequence of T
579	4	10.3	31	17	AAW03903	Glucagon like pept
580	4	10.3	31	17	AAW03971	VDJ joint protein,
581	4	10.3	31	18	AAW41134	VH251 DK1 J2 gamma
582	4	10.3	31	18	AAW33846	CDR3 sequence of T
583	4	10.3	31	18	AAW33844	CDR3 sequence of T
584	4	10.3	31	18	AAW33845	CDR3 sequence of T
585	4	10.3	31	18	AAW17085	Foot and mouth dis
586	4	10.3	31	18	AAW12463	Control peptide si
587	4	10.3	31	18	AAW19976	Fibronectin fragme
588	4	10.3	31	19	AAW72581	Zea mays soluble s
589	4	10.3	31	19	AAW40009	Peptide effecting
590	4	10.3	31	19	AAW39981	Peptide effecting
591	4	10.3	31	19	AAW39787	Synthetic peptide
592	4	10.3	31	20	AAY40402	Amino acid sequenc
593	4	10.3	31	20	AAY36384	Fragment of human
594	4	10.3	31	20	AAY07948	Human secreted pro
595	4	10.3	31	20	AAY12905	Human 5' EST secre
596	4	10.3	31	20	AAY12350	Human 5' EST secre
597	4	10.3	31	20	AAY11996	Human 5' EST secre
598	4	10.3	31	20	AAY11630	Human 5' EST secre
599	4	10.3	31	20	AAY10862	Amino acid sequenc
600	4	10.3	31	20	AAW88668	Secreted protein e
601	4	10.3	31	20	AAW73494	Cellobiose phospho
602	4	10.3	31	20	AAW82987	Human fibronectin
603	4	10.3	31	21	AAB28325	Human secreted pep
604	4	10.3	31	21	AAB27918	Human secreted pro
605	4	10.3	31	21	AAB39011	Human secreted pep
606	4	10.3	31	21	AAB39082	Human secreted pro
607	4	10.3	31	21	AAB15490	TCR beta V-N-J reg
608	4	10.3	31	21	AAB15491	TCR beta V-N-J reg
609	4	10.3	31	21	AAB15704	Mitochondrial matr
610	4	10.3	31	21	AAB22012	Human V gene Vbeta
611	4	10.3	31	21	AAB22037	Peptide #3 contain
612	4	10.3	31	21	AAB22041	Molecular velcro p
613	4	10.3	31	21	AAB22043	Peptide #2 contain
614	4	10.3	31	21	AAB22045	PKA peptide #1. U
615	4	10.3	31	21	AAB22835	Mitochondrial matr
616	4	10.3	31	21	AAG21998	Arabidopsis thalia
617	4	10.3	31	21	AAY70895	N-terminal portion
618	4	10.3	31	21	AAY70918	N-terminal portion
619	4	10.3	31	21	AAY54388	Amino acid sequenc
620	4	10.3	31	21	AAY54396	Amino acid sequenc

621	4	10.3	31	21	AAV54404	Amino acid sequenc
622	4	10.3	31	21	AAV67667	Peptide #67 for de
623	4	10.3	31	21	AAV67668	Peptide #68 for de
624	4	10.3	31	21	AAV67669	Peptide #69 for de
625	4	10.3	31	21	AAV67670	Peptide #70 for de
626	4	10.3	31	21	AAV67704	Peptide #104 for d
627	4	10.3	31	21	AAV67705	Peptide #105 for d
628	4	10.3	31	21	AAV67706	Peptide #106 for d
629	4	10.3	31	21	AAV67707	Peptide #107 for d
630	4	10.3	31	21	AAV67740	Peptide #140 for d
631	4	10.3	31	21	AAV67741	Peptide #141 for d
632	4	10.3	31	21	AAV67742	Peptide #142 for d
633	4	10.3	31	21	AAV67743	Peptide #143 for d
634	4	10.3	31	21	AAV67778	Peptide #178 for d
635	4	10.3	31	21	AAV67779	Peptide #179 for d
636	4	10.3	31	21	AAV67780	Peptide #180 for d
637	4	10.3	31	21	AAV55087	C. trachomatis maj
638	4	10.3	31	21	AAV65000	Human 5' EST relat
639	4	10.3	31	22	ABG49117	Human liver peptid
640	4	10.3	31	22	ABG50769	Human liver peptid
641	4	10.3	31	22	ABG53284	Human liver peptid
642	4	10.3	31	22	ABG53386	Human liver peptid
643	4	10.3	31	22	ABG55017	Human liver peptid
644	4	10.3	31	22	ABG26988	Novel human diagno
645	4	10.3	31	22	ABB29115	Peptide #1766 enco
646	4	10.3	31	22	ABB30734	Peptide #3385 enco
647	4	10.3	31	22	ABB34276	Peptide #1782 enco
648	4	10.3	31	22	ABB35909	Peptide #3415 enco
649	4	10.3	31	22	ABB38458	Peptide #5964 enco
650	4	10.3	31	22	ABB38543	Peptide #6049 enco
651	4	10.3	31	22	ABB39891	Peptide #7397 enco
652	4	10.3	31	22	ABB50435	Human secreted pro
653	4	10.3	31	22	ABB19708	Protein #1707 enco
654	4	10.3	31	22	ABB21319	Protein #3318 enco
655	4	10.3	31	22	ABB23622	Protein #5621 enco
656	4	10.3	31	22	AAB35489	Internalising pept
657	4	10.3	31	22	AAM55069	Human brain expres
658	4	10.3	31	22	AAM56714	Human brain expres
659	4	10.3	31	22	AAM59069	Human brain expres
660	4	10.3	31	22	AAM59166	Human brain expres
661	4	10.3	31	22	AAM60631	Human brain expres
662	4	10.3	31	22	AAM67462	Human bone marrow
663	4	10.3	31	22	AAM69089	Human bone marrow
664	4	10.3	31	22	AAM71602	Human bone marrow
665	4	10.3	31	22	AAM71701	Human bone marrow
666	4	10.3	31	22	AAM73303	Human bone marrow
667	4	10.3	31	22	AAM15284	Peptide #1718 enco
668	4	10.3	31	22	AAM16927	Peptide #3361 enco
669	4	10.3	31	22	AAM19230	Peptide #5664 enco
670	4	10.3	31	22	AAM27753	Peptide #1790 enco
671	4	10.3	31	22	AAM29412	Peptide #3449 enco
672	4	10.3	31	22	AAM31899	Peptide #5936 enco
673	4	10.3	31	22	AAM31993	Peptide #6030 enco
674	4	10.3	31	22	AAM33503	Peptide #7540 enco
675	4	10.3	31	22	AAM03033	Peptide #1715 enco
676	4	10.3	31	22	AAM04621	Peptide #3303 enco
677	4	10.3	31	22	AAG77415	Human colon cancer

678	4	10.3	31	22	AAB64588	Human secreted pro
679	4	10.3	31	23	ABP56034	Histidine-tagged p
680	4	10.3	31	23	ABG78091	ITALY, LOR-2, STRI
681	4	10.3	31	23	AAE23925	Human TCR Vbeta17
682	4	10.3	31	23	ABJ01053	Human breast speci
683	4	10.3	31	23	ABG37080	Human peptide enco
684	4	10.3	31	23	ABG38688	Human peptide enco
685	4	10.3	31	23	ABG41414	Human peptide enco
686	4	10.3	31	23	ABG41515	Human peptide enco
687	4	10.3	31	23	ABG43154	Human peptide enco
688	4	10.3	31	23	ABP41445	Human ovarian anti
689	4	10.3	31	23	AAM52295	Miniature protein
690	4	10.3	31	23	AAM52296	Miniature protein
691	4	10.3	31	23	AAM52297	Miniature protein
692	4	10.3	31	23	AAM52298	Miniature protein
693	4	10.3	31	24	ABR00985	Human gene 39-enco
694	4	10.3	31	24	AAG79906	KIAA1819 minimal N
695	4	10.3	31	24	ABP99511	Human secreted pro
696	4	10.3	31	24	ABR00821	Bioactive syntheti
697	4	10.3	31	24	ABP79892	N. gonorrhoeae ami
698	4	10.3	32	12	AAR13836	Mutant signal pept
699	4	10.3	32	13	AAR23648	Antiviral peptide
700	4	10.3	32	15	AAR48260	Mitochondrial matr
701	4	10.3	32	15	AAR57988	B. licheniformis a
702	4	10.3	32	16	AAR74060	Superantigen pepti
703	4	10.3	32	19	AAW66430	Cationic peptide R
704	4	10.3	32	19	AAW66431	Cationic peptide R
705	4	10.3	32	20	AAY39980	MMTV ORF(245-276)
706	4	10.3	32	20	AAW96358	Mitochondrial matr
707	4	10.3	32	20	AAY02681	Human secreted pro
708	4	10.3	32	20	AAY12359	Human 5' EST secre
709	4	10.3	32	20	AAY12064	Human 5' EST secre
710	4	10.3	32	20	AAW78165	Human secreted pro
711	4	10.3	32	20	AAW73207	Rat defensin-2 pep
712	4	10.3	32	21	AAB39009	Human secreted pep
713	4	10.3	32	21	AAB28704	Human secreted pro
714	4	10.3	32	21	AAB10431	Rat pathogenic pri
715	4	10.3	32	21	AAG55998	Arabidopsis thalia
716	4	10.3	32	21	AAV91729	Cationic peptide R
717	4	10.3	32	21	AAV91730	Cationic peptide R
718	4	10.3	32	21	AAV58894	Polyketide polylin
719	4	10.3	32	21	AAV54389	Amino acid sequenc
720	4	10.3	32	21	AAV54397	Amino acid sequenc
721	4	10.3	32	21	AAV54405	Amino acid sequenc
722	4	10.3	32	22	ABG47791	Human liver peptid
723	4	10.3	32	22	ABG50306	Human liver peptid
724	4	10.3	32	22	AAG77848	Mouse CXCR3 chemok
725	4	10.3	32	22	ABG00577	Novel human diagno
726	4	10.3	32	22	ABG21782	Novel human diagno
727	4	10.3	32	22	ABG26119	Novel human diagno
728	4	10.3	32	22	AAG65882	B. licheniformis a
729	4	10.3	32	22	ABB27768	Human peptide #419
730	4	10.3	32	22	ABB32939	Peptide #445 encod
731	4	10.3	32	22	ABB35446	Peptide #2952 enco
732	4	10.3	32	22	ABB18416	Protein #415 encod
733	4	10.3	32	22	ABB20885	Protein #2884 enco
734	4	10.3	32	22	AAG65199	Human immunodefici

735	4	10.3	32	22	AAG65200	Simian immunodefic
736	4	10.3	32	22	AAM53740	Human brain expres
737	4	10.3	32	22	AAM56270	Human brain expres
738	4	10.3	32	22	AAM66123	Human bone marrow
739	4	10.3	32	22	AAM89561	Human immune/haema
740	4	10.3	32	22	AAM92756	Human digestive sy
741	4	10.3	32	22	AAE06938	Human membrane-typ
742	4	10.3	32	22	AAM13994	Peptide #428 encod
743	4	10.3	32	22	AAM16459	Peptide #2893 enco
744	4	10.3	32	22	AAM26400	Peptide #437 encod
745	4	10.3	32	22	AAM01735	Peptide #417 encod
746	4	10.3	32	22	AAM04188	Peptide #2870 enco
747	4	10.3	32	23	ABG92993	Localisation seque
748	4	10.3	32	23	ABG30856	Human ornithine tr
749	4	10.3	32	23	ABG35773	Human peptide enco
750	4	10.3	32	23	ABB80704	Mouse CXCR3 derive
751	4	10.3	32	23	ABP27640	Streptococcus poly
752	4	10.3	32	23	AAU91012	Transplant media a
753	4	10.3	32	23	AAU91045	Transplant media a
754	4	10.3	32	23	AAU70444	Mouse light chain
755	4	10.3	32	23	AAG80163	TPR1 protein fragm
756	4	10.3	32	23	AAG80165	TPR2B protein frag
757	4	10.3	32	23	AAU69725	Cell death protect
758	4	10.3	32	24	ABR01103	Human gene 157-enc
759	4	10.3	32	24	ABU59606	Cationic cancer -t
760	4	10.3	32	24	ABU59607	Cationic cancer -t
761	4	10.3	32	24	ABP56588	Mitochondrial matr
762	4	10.3	32	24	ABP60612	Rat insulin recept
763	4	10.3	32	24	ABP99621	Human secreted pro
764	4	10.3	32	24	ABP77933	N. gonorrhoeae ami
765	4	10.3	32	24	ABP78019	N. gonorrhoeae ami
766	4	10.3	32	24	ABU02632	S. pneumoniae type
767	4	10.3	33	10	AAP92273	Peptide PF19 from
768	4	10.3	33	11	AAR06628	Bridging sequence
769	4	10.3	33	14	AAR33102	Human cytomegalovi
770	4	10.3	33	16	AAR82896	Human B7-1 signal
771	4	10.3	33	16	AAR70265	Partial IGF-I fusi
772	4	10.3	33	18	AAW18069	Soluble starch syn
773	4	10.3	33	19	AAW66429	Cationic peptide N
774	4	10.3	33	19	AAW66423	Cationic peptide M
775	4	10.3	33	19	AAW72585	SSSI maize BE-86 k
776	4	10.3	33	19	AAW41866	Peptide used in ra
777	4	10.3	33	19	AAW41867	Peptide used in ra
778	4	10.3	33	20	AAY11807	Human 5' EST secre
779	4	10.3	33	20	AAW73202	Rabbit defensin-2
780	4	10.3	33	21	AAB56648	Human prostate can
781	4	10.3	33	21	AAB56936	Human prostate can
782	4	10.3	33	21	AAB27914	Human secreted pro
783	4	10.3	33	21	AAB38653	HIV-1 peptide epit
784	4	10.3	33	21	AAB38654	HIV-1 peptide epit
785	4	10.3	33	21	AAB38655	HIV-1 peptide epit
786	4	10.3	33	21	AAB38656	HIV-1 peptide epit
787	4	10.3	33	21	AAB38657	HIV-1 peptide epit
788	4	10.3	33	21	AAB38658	HIV-1 peptide epit
789	4	10.3	33	21	AAB38960	HIV-1 peptide epit
790	4	10.3	33	21	AAB45354	Human secreted pro
791	4	10.3	33	21	AAB15479	TCR beta V-N-J reg

792	4	10.3	33	21	AAB28706	Human secreted pro
793	4	10.3	33	21	AAB12207	Partial sequence o
794	4	10.3	33	21	AAB12209	Partial sequence o
795	4	10.3	33	21	AAB12210	Partial sequence o
796	4	10.3	33	21	AAB12211	Partial sequence o
797	4	10.3	33	21	AAB12212	Partial sequence o
798	4	10.3	33	21	AAB12213	Partial sequence o
799	4	10.3	33	21	AAB12214	Partial sequence o
800	4	10.3	33	21	AAB12215	Partial sequence o
801	4	10.3	33	21	AAB12216	Partial sequence o
802	4	10.3	33	21	AAB12217	Partial sequence o
803	4	10.3	33	21	AAB12218	Partial sequence o
804	4	10.3	33	21	AAB12220	Partial sequence o
805	4	10.3	33	21	AAB12221	Partial sequence o
806	4	10.3	33	21	AAB12222	Partial sequence o
807	4	10.3	33	21	AAB12224	Partial sequence o
808	4	10.3	33	21	AAB12225	Partial sequence o
809	4	10.3	33	21	AAB12227	Partial sequence o
810	4	10.3	33	21	AAB12228	Partial sequence o
811	4	10.3	33	21	AAB12231	Partial sequence o
812	4	10.3	33	21	AAB12233	Partial sequence o
813	4	10.3	33	21	AAB12234	Partial sequence o
814	4	10.3	33	21	AAB12235	Partial sequence o
815	4	10.3	33	21	AAB12236	Partial sequence o
816	4	10.3	33	21	AYY91722	Cationic peptide M
817	4	10.3	33	21	AYY91728	Cationic peptide N
818	4	10.3	33	21	AYY79839	HIV infection dete
819	4	10.3	33	21	AYY54390	Amino acid sequenc
820	4	10.3	33	21	AYY54398	Amino acid sequenc
821	4	10.3	33	21	AYY54406	Amino acid sequenc
822	4	10.3	33	21	AYY67712	Peptide #112 for d
823	4	10.3	33	21	AYY53944	Peptide representi
824	4	10.3	33	21	AYY56366	Mycobacterium tube
825	4	10.3	33	21	AYY65922	Transcription fact
826	4	10.3	33	22	ABG49373	Human liver peptid
827	4	10.3	33	22	ABG51491	Human liver peptid
828	4	10.3	33	22	ABG52572	Human liver peptid
829	4	10.3	33	22	ABG53813	Human liver peptid
830	4	10.3	33	22	AAU97938	pET20LSCasp3 relat
831	4	10.3	33	22	ABG18683	Novel human diagno
832	4	10.3	33	22	ABG26205	Novel human diagno
833	4	10.3	33	22	ABB29379	Peptide #2030 enco
834	4	10.3	33	22	ABB31428	Peptide #4079 enco
835	4	10.3	33	22	ABB31514	Peptide #4165 enco
836	4	10.3	33	22	ABB34552	Peptide #2058 enco
837	4	10.3	33	22	ABB36641	Peptide #4147 enco
838	4	10.3	33	22	ABB36725	Peptide #4231 enco
839	4	10.3	33	22	ABB37708	Peptide #5214 enco
840	4	10.3	33	22	ABB38907	Peptide #6413 enco
841	4	10.3	33	22	ABB19960	Protein #1959 enco
842	4	10.3	33	22	ABB21975	Protein #3974 enco
843	4	10.3	33	22	ABB23900	Protein #5899 enco
844	4	10.3	33	22	ABB03121	Human musculoskele
845	4	10.3	33	22	AAU21157	Human novel foetal
846	4	10.3	33	22	AAM55339	Human brain expres
847	4	10.3	33	22	AAM57403	Human brain expres
848	4	10.3	33	22	AAM59558	Human brain expres

849	4	10.3	33	22	AAM67735	Human bone marrow
850	4	10.3	33	22	AAM69797	Human bone marrow
851	4	10.3	33	22	AAM70809	Human bone marrow
852	4	10.3	33	22	AAM72127	Human bone marrow
853	4	10.3	33	22	AAM83263	Human immune/haema
854	4	10.3	33	22	AAM86040	Human immune/haema
855	4	10.3	33	22	AAM91722	Human immune/haema
856	4	10.3	33	22	AAO08364	Human polypeptide
857	4	10.3	33	22	AAO13724	Human polypeptide
858	4	10.3	33	22	AAM15546	Peptide #1980 enco
859	4	10.3	33	22	AAM17620	Peptide #4054 enco
860	4	10.3	33	22	AAM17702	Peptide #4136 enco
861	4	10.3	33	22	AAM18651	Peptide #5085 enco
862	4	10.3	33	22	AAM19450	Peptide #5884 enco
863	4	10.3	33	22	AAM28035	Peptide #2072 enco
864	4	10.3	33	22	AAM30138	Peptide #4175 enco
865	4	10.3	33	22	AAM30216	Peptide #4253 enco
866	4	10.3	33	22	AAM32389	Peptide #6426 enco
867	4	10.3	33	22	AAM03295	Peptide #1977 enco
868	4	10.3	33	22	AAM05278	Peptide #3960 enco
869	4	10.3	33	22	AAM05364	Peptide #4046 enco
870	4	10.3	33	22	AAM06258	Peptide #4940 enco
871	4	10.3	33	22	AAE03252	Human gene 4 encod
872	4	10.3	33	22	AAB66616	Mouse prion helix
873	4	10.3	33	22	AAB60711	Human secreted pro
874	4	10.3	33	22	AAB50220	Membrane disruptiv
875	4	10.3	33	23	ABU51880	Helicobacter pylor
876	4	10.3	33	23	AAE30590	Fruit fly odorant
877	4	10.3	33	23	ABJ01093	Ovary cell-specifi
878	4	10.3	33	23	ABG37294	Human peptide enco
879	4	10.3	33	23	ABG39426	Human peptide enco
880	4	10.3	33	23	ABG41941	Human peptide enco
881	4	10.3	33	23	AAU93751	Herpes simplex vir
882	4	10.3	33	23	AAU93752	Herpes simplex vir
883	4	10.3	33	23	AAU93753	Herpes simplex vir
884	4	10.3	33	23	AAU93754	Herpes simplex vir
885	4	10.3	33	23	AAU93755	Herpes simplex vir
886	4	10.3	33	23	AAU93756	Herpes simplex vir
887	4	10.3	33	23	AAU93757	Herpes simplex vir
888	4	10.3	33	23	AAU93758	Herpes simplex vir
889	4	10.3	33	23	AAU93759	Herpes simplex vir
890	4	10.3	33	23	AAU93760	Herpes simplex vir
891	4	10.3	33	23	AAU93761	Herpes simplex vir
892	4	10.3	33	23	AAU93762	Herpes simplex vir
893	4	10.3	33	23	AAU93763	Herpes simplex vir
894	4	10.3	33	23	AAU93764	Herpes simplex vir
895	4	10.3	33	23	AAU93765	Herpes simplex vir
896	4	10.3	33	23	AAU93766	Herpes simplex vir
897	4	10.3	33	23	AAU93767	Herpes simplex vir
898	4	10.3	33	23	AAU93768	Herpes simplex vir
899	4	10.3	33	23	AAU93769	Herpes simplex vir
900	4	10.3	33	23	AAU93770	Herpes simplex vir
901	4	10.3	33	23	AAU93771	Herpes simplex vir
902	4	10.3	33	23	AAU93772	Herpes simplex vir
903	4	10.3	33	23	AAU93773	Herpes simplex vir
904	4	10.3	33	23	AAU93774	Herpes simplex vir
905	4	10.3	33	23	AAU91007	Transplant media a

906	4	10.3	33	23	ABB05812	Amb a I MAJOR amin
907	4	10.3	33	23	ABB05813	Amb a I MINOR amin
908	4	10.3	33	23	ABB05884	Amb a I MAJOR amin
909	4	10.3	33	23	ABB05885	Amb a I MINOR amin
910	4	10.3	33	24	ABU59599	Cationic cancer -t
911	4	10.3	33	24	ABU59605	Cationic cancer -t
912	4	10.3	33	24	ABP58163	Mouse DAKAR ankyri
913	4	10.3	33	24	ABU12415	Novel human muscul
914	4	10.3	33	24	ABU00745	S. pneumoniae type
915	4	10.3	33	24	ABU01120	S. pneumoniae type
916	4	10.3	33	24	ABU01210	S. pneumoniae type
917	4	10.3	34	14	AAR44778	N-terminal sequenc
918	4	10.3	34	15	AAR45511	Parathyroid hormon
919	4	10.3	34	16	AAR85893	WD-40 consensus se
920	4	10.3	34	16	AAR83120	Thermus thermophil
921	4	10.3	34	16	AAR69041	PTH analogue with
922	4	10.3	34	17	AAY16755	Calcitonin peptide
923	4	10.3	34	17	AAR94017	Thermus thermophil
924	4	10.3	34	18	AAW35877	Leader sequence fo
925	4	10.3	34	18	AAW13338	Truncated parathy
926	4	10.3	34	18	AAW12634	Parathyroid hormon
927	4	10.3	34	18	AAW01812	Human papillomavir
928	4	10.3	34	19	AAW61713	Parathyroid hormon
929	4	10.3	34	19	AAW66039	Parathyroid hormon
930	4	10.3	34	19	AAW42585	Parathyroid hormon
931	4	10.3	34	20	AAY60170	Human endometrium
932	4	10.3	34	20	AAY41508	Fragment of human
933	4	10.3	34	20	AAY48250	Human prostate can
934	4	10.3	34	20	AAW74385	Modified parathyro
935	4	10.3	34	20	AAY00277	Human secreted pro
936	4	10.3	34	20	AAW81931	Synthetic PTH and
937	4	10.3	34	21	AAB52133	Human secreted pro
938	4	10.3	34	21	AAB39261	Gene 23 human secr
939	4	10.3	34	21	AAB44620	Human secreted pro
940	4	10.3	34	21	AAB44734	Human secreted pro
941	4	10.3	34	21	AAB38026	Fragment of human
942	4	10.3	34	21	AAB10375	HSV gD signal pept
943	4	10.3	34	21	AAB16930	Bacteriophage Dp-1
944	4	10.3	34	21	AAY92780	Vtgss-CAT fusion p
945	4	10.3	34	21	AAY58893	Polyketide polylin
946	4	10.3	34	21	AAY54391	Amino acid sequenc
947	4	10.3	34	21	AAY54399	Amino acid sequenc
948	4	10.3	34	21	AAY54407	Amino acid sequenc
949	4	10.3	34	21	AAY58292	Human p160 coactiv
950	4	10.3	34	21	AAY58295	Human p160 coactiv
951	4	10.3	34	21	AAY58298	Human p160 coactiv
952	4	10.3	34	21	AAY58335	Human Grip-1 H17A/
953	4	10.3	34	21	AAY67777	Peptide #177 for d
954	4	10.3	34	21	AAY65921	Transcription fact
955	4	10.3	34	22	ABG49025	Human liver peptid
956	4	10.3	34	22	ABG51121	Human liver peptid
957	4	10.3	34	22	ABG54406	Human liver peptid
958	4	10.3	34	22	ABG58736	Human liver peptid
959	4	10.3	34	22	ABG00686	Novel human diagno
960	4	10.3	34	22	ABG25440	Novel human diagno
961	4	10.3	34	22	ABB29022	Peptide #1673 enco
962	4	10.3	34	22	ABB34186	Peptide #1692 enco

963	4	10.3	34	22	ABB36285	Peptide #3791 enco
964	4	10.3	34	22	ABB39416	Peptide #6922 enco
965	4	10.3	34	22	ABB43350	Peptide #10856 enc
966	4	10.3	34	22	ABB43940	Peptide #11446 enc
967	4	10.3	34	22	ABB19627	Protein #1626 enco
968	4	10.3	34	22	ABB21650	Protein #3649 enco
969	4	10.3	34	22	ABB26347	Protein #8346 enco
970	4	10.3	34	22	ABB26854	Protein #8853 enco
971	4	10.3	34	22	AAM54980	Human brain expres
972	4	10.3	34	22	AAM57056	Human brain expres
973	4	10.3	34	22	AAM60097	Human brain expres
974	4	10.3	34	22	AAM64258	Human brain expres
975	4	10.3	34	22	AAM64933	Human brain expres
976	4	10.3	34	22	AAM67363	Human bone marrow
977	4	10.3	34	22	AAM69446	Human bone marrow
978	4	10.3	34	22	AAM72708	Human bone marrow
979	4	10.3	34	22	AAM77082	Human bone marrow
980	4	10.3	34	22	AAM77668	Human bone marrow
981	4	10.3	34	22	AAM84974	Human immune/haema
982	4	10.3	34	22	AAO09392	Human polypeptide
983	4	10.3	34	22	AAM15194	Peptide #1628 enco
984	4	10.3	34	22	AAM17280	Peptide #3714 enco
985	4	10.3	34	22	AAM21060	Peptide #7494 enco
986	4	10.3	34	22	AAM21588	Peptide #8022 enco
987	4	10.3	34	22	AAM27653	Peptide #1690 enco
988	4	10.3	34	22	AAM29780	Peptide #3817 enco
989	4	10.3	34	22	AAM32939	Peptide #6976 enco
990	4	10.3	34	22	AAM37204	Peptide #11241 enc
991	4	10.3	34	22	AAM37870	Peptide #11907 enc
992	4	10.3	34	22	AAM02934	Peptide #1616 enco
993	4	10.3	34	22	AAM04968	Peptide #3650 enco
994	4	10.3	34	22	AAB84639	Antigenic peptide
995	4	10.3	34	22	AAB62581	Peptide antigen cr
996	4	10.3	34	22	AAB50118	Human brain T calc
997	4	10.3	34	23	ABG70720	Human tetratricope
998	4	10.3	34	23	ABP62013	Human secreted pro
999	4	10.3	34	23	ABB79459	Gene highly expres
1000	4	10.3	34	23	ABG36994	Human peptide enco

ALIGNMENTS

RESULT 1

AAB80490

ID AAB80490 standard; Peptide; 39 AA.

XX

AC AAB80490;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 peptide #1.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;

KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.
XX
OS Bos taurus.
XX
PN WO200077042-A2.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.
XX
PR 15-JUN-1999; 99US-0139335.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.
XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
PS Claim 2; Page 16; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.
XX
SQ Sequence 39 AA;

Query Match 100.0%; Score 39; DB 22; Length 39;
Best Local Similarity 100.0%; Pred. No. 6.3e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

RESULT 2

ABB82202

ID ABB82202 standard; peptide; 39 AA.

XX

AC ABB82202;

XX

DT 23-DEC-2002 (first entry)

XX

DE TIP39 polypeptide fragment (residues 1-39).

XX

KW TIP39; parathyroid hormone-related peptide; PTHrP; TIP; osteopathic; PTH;

KW parathyroid hormone; gene therapy; PTH1R; PTH2R; hyperparathyroidism;

KW hypercalcemia; osteoporosis.

XX

OS Bos sp.

XX

PN WO200268585-A2.

XX

PD 06-SEP-2002.

XX

PF 17-JAN-2002; 2002WO-US01183.

XX

PR 17-JAN-2001; 2001US-261804P.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (JUEP/) JUEPPNER H.

PA (GARD/) GARDELLA T J.

PA (JONS/) JONSSON K P.

PA (JOHN/) JOHN M R.

PA (GENS/) GENSURE R C.

XX

PI Jueppner H, Gardella TJ, Jonsson KP, John MR, Gensure RC;

XX

DR WPI; 2002-713370/77.

XX

PT New truncated TIP39 polypeptides and chimeric parathyroid
PT hormone-related peptide/TIP polypeptides, useful as modulators of
PT parathyroid hormone receptors for treating e.g. hyperparathyroidism,
PT hypercalcemia or osteoporosis -

XX

PS Claim 9; Page 79; 112pp; English.

XX

CC The invention relates to truncated TIP39 polypeptide fragments and
CC chimeric parathyroid hormone-related peptide (PTHrP) receptor/TIP
CC polypeptides. The polypeptides are useful as an antagonist of PTH
CC receptors to treat conditions requiring antagonism of parathyroid hormone
CC (PTH)/PTH-related peptide (PTHrP) receptors. The TIP polypeptide is also
CC useful for treating mammalian conditions characterized by abnormality
CC related to activated PTH2R. It is also useful for treating a mammalian
CC conditions characterized by requiring antagonism of PTH1R or PTH2R (e.g.
CC hyperparathyroidism or hypercalcemia), or characterized by increases in
CC calcium resulting from excess PTH or PTHrP. The PTH1R agonist is useful
CC for treating mammalian conditions characterized by decreases in bone
CC mass, e.g. osteoporosis. The present sequence represents a TIP39
CC polypeptide fragment.

XX
SQ Sequence 39 AA;

Query Match 100.0%; Score 39; DB 23; Length 39;
Best Local Similarity 100.0%; Pred. No. 6.3e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLALADDAAFRERARLLAALERRRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 SLALADDAAFRERARLLAALERRRHWLNSYMHKLLVLDAP 39

RESULT 3
AAE23970
ID AAE23970 standard; peptide; 39 AA.
XX
AC AAE23970;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human TIP39 mature protein.
XX
KW Human; tuberoinfundibular peptide; TIP39; signal transduction;
KW parathyroid hormone 2; PTH2 receptor.
XX
OS Homo sapiens.
XX
PN WO200233049-A1.
XX
PD 25-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US31954.
XX
PR 17-OCT-2000; 2000US-241012P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Wang H, Koblan KS, Sun H, Della Penna K;
XX
DR WPI; 2002-471397/50.
DR N-PSDB; AAD38678.
XX
PT Isolated polynucleotide encoding human TIP39 peptide for identifying
PT functional TIP39 and a test compound which modulates the activity of
PT the peptide -
XX
PS Claim 9; Fig 3; 61pp; English.
XX
CC The invention relates to human tuberoinfundibular peptide (TIP39)
CC and nucleic acid molecules encoding such peptides. Polynucleotides
CC of the invention are useful in bioassays for identifying test
CC compounds that modulate the TIP39 activity. TIP39 polypeptides are
CC used for modulating the endogenous signal transducing activity of
CC parathyroid hormone 2 (PTH-2) receptor in a mammal. They are also
CC useful as diagnostics for distinguishing disease states caused by
CC a dysfunctional endogenous TIP39 or PTH-2 receptor and for screening
CC compounds in vitro to determine whether a compound functions as a

CC potential agonist or antagonist. The present sequence is human
CC TIP39 mature protein.
XX
SQ Sequence 39 AA;

Query Match 100.0%; Score 39; DB 23; Length 39;
Best Local Similarity 100.0%; Pred. No. 6.3e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

RESULT 4
ABP56764
ID ABP56764 standard; Protein; 39 AA.
XX
AC ABP56764;
XX
DT 01-APR-2003 (first entry)
XX
DE Human TIP39 protein SEQ ID NO:3.
XX
KW Human; TIP39; tuberoinfundibular peptide of 39 residues; PTH2 receptor;
KW parathyroid hormone 2 receptor; pain; analgesic; chronic pain syndrome;
KW PTH2 receptor modulator; hypersensitivity; windup; allodynia.
XX
OS Homo sapiens.
XX
PN WO2002100349-A2.
XX
PD 19-DEC-2002.
XX
PF 12-JUN-2002; 2002WO-US18771.
XX
PR 13-JUN-2001; 2001US-297959P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Usdin T;
XX
DR WPI; 2003-167369/16.
DR N-PSDB; ABZ22667.
XX
PT Ameliorating pain, e.g. chronic pain syndromes, hypersensitivity,
PT windup or allodynia, comprises administering a modulator of the
PT parathyroid hormone-2 (PTH2) receptor -
XX
PS Disclosure; Page 5; 56pp; English.
XX
CC The present invention describes a method for ameliorating pain. The
CC method comprises administering a compound that modulates a parathyroid
CC hormone-2 (PTH2) receptor to a patient. Tuberoinfundibular peptide of 39
CC residues (TIP39) selectively activates the PTH2 receptor. TIP39 has
CC analgesic activity, and can be used as a PTH2 receptor modulator. The
CC method is useful for ameliorating pain in a patient, e.g. chronic pain

PS Disclosure; Page 63; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.

XX

SQ Sequence 40 AA;

Query Match 100.0%; Score 39; DB 23; Length 40;
Best Local Similarity 100.0%; Pred. No. 6.4e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

RESULT 6

AAB80489

ID AAB80489 standard; Peptide; 38 AA.

XX

AC AAB80489;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #2.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.
XX
PN WO200077042-A2.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.
XX
PR 15-JUN-1999; 99US-0139335.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.
XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
PS Claim 5; Page 16; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

XX
SQ Sequence 38 AA;

Query Match 97.4%; Score 38; DB 22; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.8e-27;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 LALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 38

RESULT 7

AAB80526

ID AAB80526 standard; Peptide; 38 AA.

XX

AC AAB80526;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #38.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

XX

PF 15-JUN-2000; 2000WO-US16776.

XX

PR 15-JUN-1999; 99US-0139335.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Usdin TB, Hoare SRJ;

XX

DR WPI; 2001-122833/13.

XX

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

XX

PS Claim 5; Page 17; 106pp; English.

XX

CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

XX

CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

XX

SQ Sequence 37 AA;

Query Match 94.9%; Score 37; DB 22; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.7e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 ALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 37

RESULT 9

AAB80525

ID AAB80525 standard; Peptide; 37 AA.

XX

AC AAB80525;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #39.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

XX

KW hypercalcemia; osteoporosis.
XX
OS Bos sp.
XX
PN WO200268585-A2.
XX
PD 06-SEP-2002.
XX
PF 17-JAN-2002; 2002WO-US01183.
XX
PR 17-JAN-2001; 2001US-261804P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (JUEP/) JUEPPNER H.
PA (GARD/) GARDELLA T J.
PA (JONS/) JONSSON K P.
PA (JOHN/) JOHN M R.
PA (GENS/) GENSURE R C.
XX
PI Jueppner H, Gardella TJ, Jonsson KP, John MR, Gensure RC;
XX
DR WPI; 2002-713370/77.
XX
PT New truncated TIP39 polypeptides and chimeric parathyroid
PT hormone-related peptide/TIP polypeptides, useful as modulators of
PT parathyroid hormone receptors for treating e.g. hyperparathyroidism,
PT hypercalcemia or osteoporosis -
XX
PS Claim 1; Page 78; 112pp; English.
XX
CC The invention relates to truncated TIP39 polypeptide fragments and
CC chimeric parathyroid hormone-related peptide (PTHrP) receptor/TIP
CC polypeptides. The polypeptides are useful as an antagonist of PTH
CC receptors to treat conditions requiring antagonism of parathyroid hormone
CC (PTH)/PTH-related peptide (PTHrP) receptors. The TIP polypeptide is also
CC useful for treating mammalian conditions characterized by abnormality
CC related to activated PTH2R. It is also useful for treating a mammalian
CC conditions characterized by requiring antagonism of PTH1R or PTH2R (e.g.
CC hyperparathyroidism or hypercalcemia), or characterized by increases in
CC calcium resulting from excess PTH or PTHrP. The PTH1R agonist is useful
CC for treating mammalian conditions characterized by decreases in bone
CC mass, e.g. osteoporosis. The present sequence represents a truncated
CC TIP39 polypeptide fragment.
XX
SQ Sequence 37 AA;

Query Match 94.9%; Score 37; DB 23; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.7e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
| || || || || || || || || || || || || || || || |
Db 1 ALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 37

RESULT 11
AAB80487

ID AAB80487 standard; Peptide; 36 AA.
XX
AC AAB80487;
XX
DT 26-APR-2001 (first entry)
XX
DE PTH2 receptor binding activity TIP39 truncation peptide #4.
XX
KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.
XX
OS Bos taurus.
OS Synthetic.
XX
PN WO200077042-A2.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.
XX
PR 15-JUN-1999; 99US-0139335.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.
XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
PS Claim 5; Page 16; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating

CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

XX

SQ Sequence 36 AA;

Query Match 92.3%; Score 36; DB 22; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.9e-25;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 LADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 36

RESULT 12

AAB80524

ID AAB80524 standard; Peptide; 36 AA.

XX

AC AAB80524;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #40.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

XX

PF 15-JUN-2000; 2000WO-US16776.

XX

PR 15-JUN-1999; 99US-0139335.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Usdin TB, Hoare SRJ;

XX

DR WPI; 2001-122833/13.

XX

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

XX
PS Claim 5; Page 17; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.
XX

SQ Sequence 36 AA;

Query Match 92.3%; Score 36; DB 22; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.9e-25;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVL 36
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVL 36

RESULT 13

AAB80486
ID AAB80486 standard; Peptide; 35 AA.

XX
AC AAB80486;

XX
DT 26-APR-2001 (first entry)

XX
DE PTH2 receptor binding activity TIP39 truncation peptide #5.

XX
KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX
OS Bos taurus.
OS Synthetic.
XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

XX

PF 15-JUN-2000;

xx 15 JUL 1986 20UG 0120325

PR 15-JUN-1999;
VV

PA (LICCU) UC DEPT HEALTH & HUMAN SERVICES

XX (055H), 05 B
YY

PI Usdin TB Hoare SBT:

xx

DR WPI; 2001-122833/13.

XX

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

XX

PS Claim 5; Page 16; 106pp; English.

XX

The present invention describes an isolated or purified peptide (I) that is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1 receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression, nootropic, analgesic, antimigraine, antidiabetic, osteopathic, hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective activities, and is an PTH receptor antagonist. The peptide is useful in the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor. The PTH2 receptor binding activity may be used in treating obesity or other eating or metabolic disorders, mental disorders (e.g. depression, schizophrenia and dementia), acute or chronic pain, migraine or headaches, diabetes and other metabolic disorders, osteoporosis, hypercalcaemia and other disorders affecting calcium metabolism, hypertension, congestive heart failure and control of tumour growth, asthma, emphysema or other restrictive lung diseases, and demyelinating conditions such as multiple sclerosis and leukodystrophies. AAB80454 to AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues) truncated peptides which have PTH2 receptor binding activity.

xx

Query Match 89.7%; Score 35; DB 22;

Best Local Similarity 100.0%; Pred. No. 2.2e-24;

Qy 5 ADDAAFRERARLLAALERRHWLNSYMHKLVLDAE

Ph. 1. MERRIFERD BILLY ALFREDIEUNGUMVILLE DAB. 35

RESULT 14

AAB80523

ID AAB80523 standard: Peptide: 35 AA.

xx

AC AAB80523;

xx

DT 26-APR-2001

DE PTH2 receptor binding activity TIP39 truncation peptide #41.
XX
KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.
XX
OS Bos taurus.
OS Synthetic.
XX
PN WO200077042-A2.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.
XX
PR 15-JUN-1999; 99US-0139335.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.
XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
PS Claim 5; Page 17; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.
XX
SQ Sequence 35 AA;

Query Match 89.7%; Score 35; DB 22; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.2e-24;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLV 35
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLV 35

RESULT 15

AAB80527

ID AAB80527 standard; Peptide; 35 AA.

XX

AC AAB80527;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #74.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

XX

PF 15-JUN-2000; 2000WO-US16776.

XX

PR 15-JUN-1999; 99US-0139335.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Usdin TB, Hoare SRJ;

XX

DR WPI; 2001-122833/13.

XX

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

XX

PS Claim 6; Page 17; 106pp; English.

XX

CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,

CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

XX
SQ Sequence 35 AA;

Query Match 89.7%; Score 35; DB 22; Length 35;
 Best Local Similarity 100.0%; Pred. No. 2.e-24;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
| | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 ADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 35

RESULT 16

AAB80485

ID AAB80485 standard; Peptide; 34 AA.

XX

AC AAB80485;

xx
ETC 26.1 PP. 2661 (5) (1970)

DI 26-APR-20
XX

DE PTH2 receptor binding activity TIP39 truncation peptide #6

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS *Bos taurus*

OS Synthetic

xx

PN WO200077042-A2 .

xx 21 DEC 20

FD 21-DEC-2000.
VV

PE 15-JUN-20

xx

PR 15-JUN-1999; 99US-0139335.

XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PT Ustdin TB, Hoare SRJ:

XX
DR WPT: 2001-122833/13.

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

ES Claim 5: Page 16: 106pp; English.

XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

SO Sequence 34 AA:

Query Match 87.2%; Score 34; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	6	DDAAFRERARLLAALERRHWLNNSYMHKLLVLDAP	39
Db	1	DDAAFRERARLLAALERRHWLNNSYMHKLLVLDAP	34

RESULT 17

AAB80522

ID AAB80522 standard; Peptide; 34 AA.

XX

AC AAB80522;

XX

DT 26-APR-2001 (first entry)

二二

DE PTH2 receptor binding activity RFP39 truncation peptide #42.

XX

RW tuberin/hindbrain peptide of 35 residues, PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;

KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.
XX
OS Bos taurus.
OS Synthetic.
XX
PN WO200077042-A2.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.
XX
PR 15-JUN-1999; 99US-0139335.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.
XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
PS Claim 5; Page 17; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.
XX
SQ Sequence 34 AA;

Query Match 87.2%; Score 34; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLL 34
|||||||||||||||||||||||||||||||||

Db

1 SLALADDAAFRERARLLAALERRHWLNSYMHKLL 34

RESULT 18

AAB80528

ID AAB80528 standard; Peptide; 34 AA.

XX

AC AAB80528;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #75.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

XX

PF 15-JUN-2000; 2000WO-US16776.

XX

PR 15-JUN-1999; 99US-0139335.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Usdin TB, Hoare SRJ;

XX

DR WPI; 2001-122833/13.

XX

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

XX

PS Claim 6; Page 17; 106pp; English.

XX

CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,

CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

XX
SQ

```

Query Match           87.2%;  Score 34;  DB 22;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 1.7e-23;
Matches   34;  Conservative    0;  Mismatches    0;  Indels     0;  Gaps     0;

```

Qy	6	DDAAFRRRARLLAALERRHWLNSYMHKLVLVDAP	39
Db	1	DDAAFRRRARLLAALERRHWLNSYMHKLVLVDAP	34

RESULT 19

AAB80484

ID AAB80484 standard; Peptide; 33 AA.

xx

AC AAB80484 ;

xx

DT 26-APR-2001 (first entry)

xx

DE PTH2 receptor binding activity TIP39 truncation peptide #7.

xx

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

xx

OS *Bos taurus*.

OS Synthetic.

xx

PN WO200077042-A2.

xx

PD 21-DEC-2000.

xx

PF 15-JUN-2000; 2000WO-US16776.

xx

PR 15-JUN-1999; 99US-0139335.

xx

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

xx

PI Usdin TB, Hoare SRJ;

xx

DR WPI; 2001-122833/13.

XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

PS Claim 5: Page 16: 106pp: English.

XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

xx
SO Sequence 33 AA:

Query Match 84.6%; Score 33; DB 22; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.3e-22;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DAAFRERARLLAALERRHWLNSYMHKLVLVDAP 39
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAAFRERARLLAALERRHWLNSYMHKLVLVDAP 33

RESULT 20

AAB80521

ID AAB80521 standard; Peptide; 33 AA.

XX

AC

xx 2010-0001 (51 pages)

100

PTU2 receptor binding activity TIP39 truncation peptide #43

DE
VV

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;

KW leukodystrophy.
XX
OS Bos taurus.
OS Synthetic.
XX
PN WO200077042-A2.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.
XX
PR 15-JUN-1999; 99US-0139335.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.
XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
PS Claim 5; Page 17; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.
XX
SQ Sequence 33 AA;

Query Match 84.6%; Score 33; DB 22; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKL 33
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKL 33

RESULT 21
AAB80529
ID AAB80529 standard; Peptide; 33 AA.

XX
AC AAB80529;
XX
DT 26-APR-2001 (first entry)
XX
DE PTH2 receptor binding activity TIP39 truncation peptide #76.
XX
KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.
XX
OS Bos taurus.
OS Synthetic.
XX
PN WO200077042-A2.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.
XX
PR 15-JUN-1999; 99US-0139335.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.
XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
PS Claim 6; Page 17; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is a PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to

CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.
XX
SQ Sequence 33 AA;
Query Match 84.6%; Score 33; DB 22; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 DAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 DAAFRERARLLAALERRHWLNSYMHKLLVLDAP 33

RESULT 22
AAB80483
ID AAB80483 standard; Peptide; 32 AA.
XX
AC AAB80483;
XX
DT 26-APR-2001 (first entry)
XX
DE PTH2 receptor binding activity TIP39 truncation peptide #8.
XX
KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.
XX
OS Bos taurus.
OS Synthetic.
XX
PN WO200077042-A2.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.
XX
PR 15-JUN-1999; 99US-0139335.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.
XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX

PS Claim 5; Page 16; 106pp; English.

XX

CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

XX

SQ Sequence 32 AA;

Query Match 82.1%; Score 32; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 9.9e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 AAFRERARLLAALERRHWLNSYMHKLLVLDAP 32

RESULT 23

AAB80520

ID AAB80520 standard; Peptide; 32 AA.

XX

AC AAB80520;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #44.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.
XX
PR 15-JUN-1999; 99US-0139335.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.
XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
PS Claim 5; Page 17; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.
XX
SQ Sequence 32 AA;

Query Match 82.1%; Score 32; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 9.9e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHK 32
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHK 32

RESULT 24
AAB80530
ID AAB80530 standard; Peptide; 32 AA.
XX
AC AAB80530;
XX
DT 26-APR-2001 (first entry)
XX
DE PTH2 receptor binding activity TIP39 truncation peptide #77.

XX
KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.
XX
OS Bos taurus.
OS Synthetic.
XX
PN WO200077042-A2.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.
XX
PR 15-JUN-1999; 99US-0139335.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.
XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
PS Claim 6; Page 18; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.
XX
SQ Sequence 32 AA;

Best Local Similarity 100.0%; Pred. No. 9.9e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 AAFRERARLLAALERRHWLNSYMHKLLVLDAP 32

RESULT 25

ABB82198

ID ABB82198 standard; peptide; 32 AA.

XX

AC ABB82198;

XX

DT 23-DEC-2002 (first entry)

XX

DE TIP39 truncated peptide fragment (residues 8-39).

XX

KW TIP39; parathyroid hormone-related peptide; PTHrP; TIP; osteopathic; PTH;

KW parathyroid hormone; gene therapy; PTH1R; PTH2R; hyperparathyroidism;

KW hypercalcemia; osteoporosis.

XX

OS Bos sp.

XX

PN WO200268585-A2.

XX

PD 06-SEP-2002.

XX

PF 17-JAN-2002; 2002WO-US01183.

XX

PR 17-JAN-2001; 2001US-261804P.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (JUEP/) JUEPPNER H.

PA (GARD/) GARDELLA T J.

PA (JONS/) JONSSON K P.

PA (JOHN/) JOHN M R.

PA (GENS/) GENSURE R C.

XX

PI Jueppner H, Gardella TJ, Jonsson KP, John MR, Gensure RC;

XX

DR WPI; 2002-713370/77.

XX

PT New truncated TIP39 polypeptides and chimeric parathyroid
PT hormone-related peptide/TIP polypeptides, useful as modulators of
PT parathyroid hormone receptors for treating e.g. hyperparathyroidism,
PT hypercalcemia or osteoporosis -

XX

PS Claim 2; Page 78; 112pp; English.

XX

CC The invention relates to truncated TIP39 polypeptide fragments and
CC chimeric parathyroid hormone-related peptide (PTHrP) receptor/TIP
CC polypeptides. The polypeptides are useful as an antagonist of PTH
CC receptors to treat conditions requiring antagonism of parathyroid hormone
CC (PTH)/PTH-related peptide (PTHrP) receptors. The TIP polypeptide is also
CC useful for treating mammalian conditions characterized by abnormality
CC related to activated PTH2R. It is also useful for treating a mammalian

CC conditions characterized by requiring antagonism of PTH1R or PTH2R (e.g.
CC hyperparathyroidism or hypercalcemia), or characterized by increases in
CC calcium resulting from excess PTH or PTHrP. The PTH1R agonist is useful
CC for treating mammalian conditions characterized by decreases in bone
CC mass, e.g. osteoporosis. The present sequence represents a truncated
CC TIP39 polypeptide fragment.

XX

SQ Sequence 32 AA;

Query Match 82.1%; Score 32; DB 23; Length 32;
Best Local Similarity 100.0%; Pred. No. 9.9e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 AAFRERARLLAALERRHWLNSYMHKLLVLDAP 32

RESULT 26

AAB80482

ID AAB80482 standard; Peptide; 31 AA.

XX

AC AAB80482;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #9.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

XX

PF 15-JUN-2000; 2000WO-US16776.

XX

PR 15-JUN-1999; 99US-0139335.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Usdin TB, Hoare SRJ;

XX

DR WPI; 2001-122833/13.

XX

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

XX
PS Claim 5; Page 16; 106pp; English.

The present invention describes an isolated or purified peptide (I) that is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1 receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression, nootropic, analgesic, antimigraine, antidiabetic, osteopathic, hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective activities, and is an PTH receptor antagonist. The peptide is useful in the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor. The PTH2 receptor binding activity may be used in treating obesity or other eating or metabolic disorders, mental disorders (e.g. depression, schizophrenia and dementia), acute or chronic pain, migraine or headaches, diabetes and other metabolic disorders, osteoporosis, hypercalcaemia and other disorders affecting calcium metabolism, hypertension, congestive heart failure and control of tumour growth, asthma, emphysema or other restrictive lung diseases, and demyelinating conditions such as multiple sclerosis and leukodystrophies. AAB80454 to AAB80558 represent TIP39' (tuberinfundibular peptide of 39 residues) truncated peptides which have PTH2 receptor binding activity.

XX SO Sequence 31 AA:

```

Query Match          79.5%;  Score 31;  DB 22;  Length 31;
Best Local Similarity 100.0%;  Pred. No. 7.6e-21;
Matches    31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Y      9 AFRERARLLAALERRH WLNSYMHKLLVLDAP 39
       ||||||| | | | | | | | | | | | | | | | |
D      1 AFRERARLLAALERRH WLNSYMHKLLVLDAP 31

```

RESULT 27

AAB80519

ID AAB80519 standard; Peptide; 31 AA.

XX

AC AAB80519;

xx

DT 26-APR-2001 (first entry)

xx

DE PTH2 receptor binding activity TIP39 truncation peptide #45.

xx

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

xx

OS Bos taurus.
OS Synthetic.
XX
PN WO200077042-A2.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.
XX
PR 15-JUN-1999; 99US-0139335.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.
XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
PS Claim 5; Page 17; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.
XX
SQ Sequence 31 AA;

Query Match 79.5%; Score 31; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.6e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMH 31
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMH 31

RESULT 28
AAB80531
ID AAB80531 standard; Peptide; 31 AA.
XX
AC AAB80531;

XX
DT 26-APR-2001 (first entry)
XX
DE PTH2 receptor binding activity TIP39 truncation peptide #78.
XX
KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.
XX
OS Bos taurus.
OS Synthetic.
XX
PN WO200077042-A2.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.
XX
PR 15-JUN-1999; 99US-0139335.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.
XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
PS Claim 6; Page 18; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is a PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

XX
SQ Sequence 31 AA;

Query Match 79.5%; Score 31; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.6e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AFRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| | | | | | | | | | | | | | | | | | | |
Db 1 AFRERARLLAALERRHWLNSYMHKLLVLDAP 31

RESULT 29
ABB82196
ID ABB82196 standard; peptide; 31 AA.
XX
AC ABB82196;
XX
DT 23-DEC-2002 (first entry)
XX
DE TIP39 truncated peptide fragment (residues 9-39).
XX
KW TIP39; parathyroid hormone-related peptide; PTHrP; TIP; osteopathic; PTH;
KW parathyroid hormone; gene therapy; PTH1R; PTH2R; hyperparathyroidism;
KW hypercalcemia; osteoporosis.
XX
OS Bos sp.
XX
PN WO200268585-A2.
XX
PD 06-SEP-2002.
XX
PF 17-JAN-2002; 2002WO-US01183.
XX
PR 17-JAN-2001; 2001US-261804P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (JUEP/) JUEPPNER H.
PA (GARD/) GARDELLA T J.
PA (JONS/) JONSSON K P.
PA (JOHN/) JOHN M R.
PA (GENS/) GENSURE R C.
XX
PI Jueppner H, Gardella TJ, Jonsson KP, John MR, Gensure RC;
XX
DR WPI; 2002-713370/77.
XX
PT New truncated TIP39 polypeptides and chimeric parathyroid
PT hormone-related peptide/TIP polypeptides, useful as modulators of
PT parathyroid hormone receptors for treating e.g. hyperparathyroidism,
PT hypercalcemia or osteoporosis -
XX
PS Claim 1; Page 78; 112pp; English.
XX
CC The invention relates to truncated TIP39 polypeptide fragments and
CC chimeric parathyroid hormone-related peptide (PTHrP) receptor/TIP
CC polypeptides. The polypeptides are useful as an antagonist of PTH

CC receptors to treat conditions requiring antagonism of parathyroid hormone
CC (PTH)/PTH-related peptide (PTHrP) receptors. The TIP polypeptide is also
CC useful for treating mammalian conditions characterized by abnormality
CC related to activated PTH2R. It is also useful for treating a mammalian
CC conditions characterized by requiring antagonism of PTH1R or PTH2R (e.g.
CC hyperparathyroidism or hypercalcemia), or characterized by increases in
CC calcium resulting from excess PTH or PTHrP. The PTH1R agonist is useful
CC for treating mammalian conditions characterized by decreases in bone
CC mass, e.g. osteoporosis. The present sequence represents a truncated
CC TIP39 polypeptide fragment.

XX

SQ Sequence 31 AA;

Query Match 79.5%; Score 31; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.6e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AFRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 AFRERARLLAALERRHWLNSYMHKLLVLDAP 31

RESULT 30

AAB80481

ID AAB80481 standard; Peptide; 30 AA.

XX

AC AAB80481;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #10.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

XX

PF 15-JUN-2000; 2000WO-US16776.

XX

PR 15-JUN-1999; 99US-0139335.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.
XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
PS Claim 5; Page 16; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

XX
SQ Sequence 30 AA;

Query Match 76.9%; Score 30; DB 22; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.8e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 FRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 FRERARLLAALERRHWLNSYMHKLLVLDAP 30

RESULT 31
AAB80518
ID AAB80518 standard; Peptide; 30 AA.

XX
AC AAB80518;
XX
DT 26-APR-2001 (first entry)

XX
DE PTH2 receptor binding activity TIP39 truncation peptide #46.

XX
KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;

KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX
OS Bos taurus.
OS Synthetic.

XX
PN WO200077042-A2.

XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.

XX
PR 15-JUN-1999; 99US-0139335.

XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.

XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

XX
PS Claim 5; Page 17; 106pp; English.

XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

XX
SQ Sequence 30 AA;

Query Match 76.9%; Score 30; DB 22; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.8e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYM 30
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 SLALADDAAFRERARLLAALERRHWLNSYM 30

AAB80532

ID AAB80532 standard; Peptide; 30 AA.

XX

AC AAB80532;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #79.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

XX

PF 15-JUN-2000; 2000WO-US16776.

XX

PR 15-JUN-1999; 99US-0139335.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Usdin TB, Hoare SRJ;

XX

DR WPI; 2001-122833/13.

XX

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

XX

PS Claim 6; Page 18; 106pp; English.

XX

CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,

CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

XX

SQ Sequence 30 AA;

Query Match 76.9%; Score 30; DB 22; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.8e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 FRERARLLAALERRHWLNSYMHKLLVLDAP 39
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 FRERARLLAALERRHWLNSYMHKLLVLDAP 30

RESULT 33

ABB82199

ID ABB82199 standard; peptide; 30 AA.

XX

AC ABB82199;

XX

DT 23-DEC-2002 (first entry)

XX

DE TIP39 truncated peptide fragment (residues 10-39).

XX

KW TIP39; parathyroid hormone-related peptide; PTHrP; TIP; osteopathic; PTH;
KW parathyroid hormone; gene therapy; PTH1R; PTH2R; hyperparathyroidism;
KW hypercalcemia; osteoporosis.

XX

OS Bos sp.

XX

PN WO200268585-A2.

XX

PD 06-SEP-2002.

XX

PF 17-JAN-2002; 2002WO-US01183.

XX

PR 17-JAN-2001; 2001US-261804P.

XX

PA (GEHO) GEN HOSPITAL CORP.
PA (JUEP/) JUEPPNER H.
PA (GARD/) GARDELLA T J.
PA (JONS/) JONSSON K P.
PA (JOHN/) JOHN M R.
PA (GENS/) GENSURE R C.

XX

PI Jueppner H, Gardella TJ, Jonsson KP, John MR, Gensure RC;

XX

DR WPI; 2002-713370/77.

XX

PT New truncated TIP39 polypeptides and chimeric parathyroid
PT hormone-related peptide/TIP polypeptides, useful as modulators of
PT parathyroid hormone receptors for treating e.g. hyperparathyroidism,
PT hypercalcemia or osteoporosis -

XX

PS Claim 2; Page 78; 112pp; English.

XX
CC The invention relates to truncated TIP39 polypeptide fragments and
CC chimeric parathyroid hormone-related peptide (PTHrP) receptor/TIP
CC polypeptides. The polypeptides are useful as an antagonist of PTH
CC receptors to treat conditions requiring antagonism of parathyroid hormone
CC (PTH)/PTH-related peptide (PTHrP) receptors. The TIP polypeptide is also
CC useful for treating mammalian conditions characterized by abnormality
CC related to activated PTH2R. It is also useful for treating a mammalian
CC conditions characterized by requiring antagonism of PTH1R or PTH2R (e.g.
CC hyperparathyroidism or hypercalcemia), or characterized by increases in
CC calcium resulting from excess PTH or PTHrP. The PTH1R agonist is useful
CC for treating mammalian conditions characterized by decreases in bone
CC mass, e.g. osteoporosis. The present sequence represents a truncated
CC TIP39 polypeptide fragment.

XX
SQ Sequence 30 AA;

Query Match 76.9%; Score 30; DB 23; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.8e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 FRERARLLAALERRHWLNSYMHKLLVLDAP 39
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 FRERARLLAALERRHWLNSYMHKLLVLDAP 30

RESULT 34
AAB80480
ID AAB80480 standard; Peptide; 29 AA.
XX
AC AAB80480;
XX
DT 26-APR-2001 (first entry)
XX
DE PTH2 receptor binding activity TIP39 truncation peptide #11.
XX
KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.
XX
OS Bos taurus.
OS Synthetic.
XX
PN WO200077042-A2.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.
XX

PR 15-JUN-1999; 99US-0139335.

xx

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

xx

PI Usdin TB, Hoare SRJ;

xx

DR WPI; 2001-122833/13.

xx

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

xx

PS Claim 5; Page 16; 106pp; English.

xx

The present invention describes an isolated or purified peptide (I) that is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1 receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression, nootropic, analgesic, antimigraine, antidiabetic, osteopathic, hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective activities, and is an PTH receptor antagonist. The peptide is useful in the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor. The PTH2 receptor binding activity may be used in treating obesity or other eating or metabolic disorders, mental disorders (e.g. depression, schizophrenia and dementia), acute or chronic pain, migraine or headaches, diabetes and other metabolic disorders, osteoporosis, hypercalcaemia and other disorders affecting calcium metabolism, hypertension, congestive heart failure and control of tumour growth, asthma, emphysema or other restrictive lung diseases, and demyelinating conditions such as multiple sclerosis and leukodystrophies. AAB80454 to AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues) truncated peptides which have PTH2 receptor binding activity.

xx

SO Sequence 29 AA:

Query Match 74.4%; Score 29; DB 22; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.4e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

11 RERARLLAALERRHWLNSYMHKLLVLDAP 39
||||| ||||| ||||| ||||| |||||

Db 1 RERARLLAALERRHWLNSYMHKLLVLDAP 29

RESULT 35

AAB80517

ID AAB80517 standard; Peptide; 29 AA.

xx

AC AAB80517;

xx

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #47.

xx

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;

KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.
XX
OS Bos taurus.
OS Synthetic.
XX
PN WO200077042-A2.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16776.
XX
PR 15-JUN-1999; 99US-0139335.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Usdin TB, Hoare SRJ;
XX
DR WPI; 2001-122833/13.
XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
PS Claim 5; Page 17; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.
XX
SQ Sequence 29 AA;

Query Match 74.4%; Score 29; DB 22; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.4e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERHHLNSY 29
|||||||||||||||||||||||||

Db

1 SLALADDAAFRERARLIAALERRHWLNSY 29

RESULT 36

AAB80533

ID AAB80533 standard; Peptide; 29 AA.

XX

AC AAB80533;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #80.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

PD 21-DEC-2000.

XX

PF 15-JUN-2000; 2000WO-US16776.

XX

PR 15-JUN-1999; 99US-0139335.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Usdin TB, Hoare SRJ;

XX

DR WPI; 2001-122833/13.

XX

PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

XX

PS Claim 6; Page 18; 106pp; English.

XX

CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is a PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,

CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

XX
SQ Sequence 29 AA;

Query Match 74.4%; Score 29; DB 22; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.4e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERARLLAALERRHWLNSYMHKLLVLDAP 39
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 RERARLLAALERRHWLNSYMHKLLVLDAP 29

RESULT 37
ABB82200
ID ABB82200 standard; peptide; 29 AA.
XX
AC ABB82200;
XX
DT 23-DEC-2002 (first entry)
XX
DE TIP39 truncated peptide fragment (residues 11-39).
XX
KW TIP39; parathyroid hormone-related peptide; PTHrP; TIP; osteopathic; PTH;
KW parathyroid hormone; gene therapy; PTH1R; PTH2R; hyperparathyroidism;
KW hypercalcemia; osteoporosis.
XX
OS Bos sp.
XX
PN WO200268585-A2.
XX
PD 06-SEP-2002.
XX
PF 17-JAN-2002; 2002WO-US01183.
XX
PR 17-JAN-2001; 2001US-261804P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (JUEP/) JUEPPNER H.
PA (GARD/) GARDELLA T J.
PA (JONS/) JONSSON K P.
PA (JOHN/) JOHN M R.
PA (GENS/) GENSURE R C.
XX
PI Jueppner H, Gardella TJ, Jonsson KP, John MR, Gensure RC;
XX
DR WPI; 2002-713370/77.
XX
PT New truncated TIP39 polypeptides and chimeric parathyroid
PT hormone-related peptide/TIP polypeptides, useful as modulators of

PT parathyroid hormone receptors for treating e.g. hyperparathyroidism,
PT hypercalcemia or osteoporosis -

XX

PS Claim 2; Page 78; 112pp; English.

XX

CC The invention relates to truncated TIP39 polypeptide fragments and
CC chimeric parathyroid hormone-related peptide (PTHrP) receptor/TIP
CC polypeptides. The polypeptides are useful as an antagonist of PTH
CC receptors to treat conditions requiring antagonism of parathyroid hormone
CC (PTH)/PTH-related peptide (PTHrP) receptors. The TIP polypeptide is also
CC useful for treating mammalian conditions characterized by abnormality
CC related to activated PTH2R. It is also useful for treating a mammalian
CC conditions characterized by requiring antagonism of PTH1R or PTH2R (e.g.
CC hyperparathyroidism or hypercalcemia), or characterized by increases in
CC calcium resulting from excess PTH or PTHrP. The PTH1R agonist is useful
CC for treating mammalian conditions characterized by decreases in bone
CC mass, e.g. osteoporosis. The present sequence represents a truncated
CC TIP39 polypeptide fragment.

XX

SQ Sequence 29 AA;

Query Match 74.4%; Score 29; DB 23; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.4e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERARLLAALERRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 RERARLLAALERRHWLNSYMHKLLVLDAP 29

RESULT 38

AAB80479

ID AAB80479 standard; Peptide; 28 AA.

XX

AC AAB80479;

XX

DT 26-APR-2001 (first entry)

XX

DE PTH2 receptor binding activity TIP39 truncation peptide #12.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX

OS Bos taurus.

OS Synthetic.

XX

PN WO200077042-A2.

XX

KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.

XX
OS Bos taurus.
OS Synthetic.

XX
PN WO200077042-A2.

XX
PD 21-DEC-2000.

XX
PF 15-JUN-2000; 2000WO-US16776.

XX
PR 15-JUN-1999; 99US-0139335.

XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
PI Usdin TB, Hoare SRJ;

XX
DR WPI; 2001-122833/13.

XX
PT New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -

XX
PS Claim 5; Page 17; 106pp; English.

XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

XX
SQ Sequence 28 AA;

Query Match 71.8%; Score 28; DB 22; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.4e-18;

CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. AAB80454 to
CC AAB80558 represent TIP39 (tuberinfundibular peptide of 39 residues)
CC truncated peptides which have PTH2 receptor binding activity.

XX
SQ Sequence 28 AA;

Query Match 71.8%; Score 28; DB 22; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ERARLLAALERRHWLNSYMHKLLVLDAP 39
||| | | | | | | | | | | | | | | | | | | | | | | |
Db 1 ERARLLAALERRHWLNSYMHKLLVLDAP 28

Search completed: January 14, 2004, 10:34:43
Job time : 49.2991 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:59 ; Search time 13.243 Seconds
(without alignments)
124.604 Million cell updates/sec

Title: US-09-843-221A-170
Perfect score: 39
Sequence: 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 25778

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	6	15.4	28	3	US-09-041-886-53	Sequence 53, Appl
2	6	15.4	37	4	US-08-817-441-7	Sequence 7, Appl
3	6	15.4	40	3	US-08-894-699-36	Sequence 36, Appl
4	6	15.4	40	3	US-08-894-699-37	Sequence 37, Appl
5	6	15.4	40	3	US-08-894-699-39	Sequence 39, Appl
6	6	15.4	40	3	US-08-894-699-40	Sequence 40, Appl
7	6	15.4	40	3	US-08-894-699-68	Sequence 68, Appl
8	6	15.4	40	3	US-09-444-410-36	Sequence 36, Appl
9	6	15.4	40	3	US-09-444-410-37	Sequence 37, Appl
10	6	15.4	40	3	US-09-444-410-39	Sequence 39, Appl
11	6	15.4	40	3	US-09-444-410-40	Sequence 40, Appl

12	6	15.4	40	3	US-09-444-410-68	Sequence 68, Appl
13	5	12.8	28	3	US-09-041-886-37	Sequence 37, Appl
14	5	12.8	28	3	US-09-041-886-38	Sequence 38, Appl
15	5	12.8	28	3	US-09-041-886-39	Sequence 39, Appl
16	5	12.8	28	3	US-09-041-886-40	Sequence 40, Appl
17	5	12.8	28	3	US-09-041-886-54	Sequence 54, Appl
18	5	12.8	30	4	US-09-205-258-614	Sequence 614, App
19	5	12.8	32	3	US-08-786-284A-3	Sequence 3, Appli
20	5	12.8	34	3	US-08-704-856C-3	Sequence 3, Appli
21	5	12.8	34	4	US-09-242-881-3	Sequence 3, Appli
22	5	12.8	38	6	5514590-5	Patent No. 5514590
23	5	12.8	40	4	US-09-406-045-11	Sequence 11, Appl
24	4	10.3	28	1	US-07-690-300B-44	Sequence 44, Appl
25	4	10.3	28	1	US-07-789-344A-11	Sequence 11, Appl
26	4	10.3	28	1	US-07-728-221B-3	Sequence 3, Appli
27	4	10.3	28	1	US-08-276-852-13	Sequence 13, Appl
28	4	10.3	28	1	US-08-664-449-37	Sequence 37, Appl
29	4	10.3	28	1	US-08-899-575-13	Sequence 13, Appl
30	4	10.3	28	1	US-08-899-575-13	Sequence 13, Appl
31	4	10.3	28	2	US-08-458-568A-6	Sequence 6, Appli
32	4	10.3	28	3	US-08-788-231A-18	Sequence 18, Appl
33	4	10.3	28	3	US-09-348-578-3	Sequence 3, Appli
34	4	10.3	28	3	US-09-348-578-11	Sequence 11, Appl
35	4	10.3	28	3	US-09-348-578-19	Sequence 19, Appl
36	4	10.3	28	3	US-08-974-549A-166	Sequence 166, App
37	4	10.3	28	3	US-09-107-991-12	Sequence 12, Appl
38	4	10.3	28	3	US-09-041-886-42	Sequence 42, Appl
39	4	10.3	28	4	US-09-507-819-30	Sequence 30, Appl
40	4	10.3	28	4	US-09-099-041A-19	Sequence 19, Appl
41	4	10.3	28	4	US-09-245-281-19	Sequence 19, Appl
42	4	10.3	28	4	US-09-149-476-520	Sequence 520, App
43	4	10.3	28	4	US-09-699-684-3	Sequence 3, Appli
44	4	10.3	28	4	US-09-699-684-11	Sequence 11, Appl
45	4	10.3	28	4	US-09-699-684-19	Sequence 19, Appl
46	4	10.3	28	4	US-09-207-359B-19	Sequence 19, Appl
47	4	10.3	28	4	US-09-340-620A-19	Sequence 19, Appl
48	4	10.3	28	4	US-09-641-576-30	Sequence 30, Appl
49	4	10.3	28	5	PCT-US95-08743-13	Sequence 13, Appl
50	4	10.3	29	1	US-07-701-414A-12	Sequence 12, Appl
51	4	10.3	29	1	US-07-746-705A-3	Sequence 3, Appli
52	4	10.3	29	1	US-08-029-402-19	Sequence 19, Appl
53	4	10.3	29	1	US-08-066-325-61	Sequence 61, Appl
54	4	10.3	29	1	US-08-066-325-74	Sequence 74, Appl
55	4	10.3	29	1	US-08-066-325-75	Sequence 75, Appl
56	4	10.3	29	1	US-07-960-510-4	Sequence 4, Appli
57	4	10.3	29	1	US-07-960-510-5	Sequence 5, Appli
58	4	10.3	29	1	US-07-960-510-6	Sequence 6, Appli
59	4	10.3	29	1	US-07-960-510-7	Sequence 7, Appli
60	4	10.3	29	2	US-08-459-568-46	Sequence 46, Appl
61	4	10.3	29	2	US-08-459-568-48	Sequence 48, Appl
62	4	10.3	29	2	US-08-399-411-46	Sequence 46, Appl
63	4	10.3	29	2	US-08-399-411-48	Sequence 48, Appl
64	4	10.3	29	2	US-08-380-182-2	Sequence 2, Appli
65	4	10.3	29	2	US-08-859-201-15	Sequence 15, Appl
66	4	10.3	29	2	US-08-859-201-23	Sequence 23, Appl
67	4	10.3	29	2	US-08-280-864A-4	Sequence 4, Appli
68	4	10.3	29	3	US-08-516-859A-46	Sequence 46, Appl

69	4	10.3	29	3	US-08-516-859A-48	Sequence 48, Appl
70	4	10.3	29	3	US-08-641-873-10	Sequence 10, Appl
71	4	10.3	29	3	US-09-348-578-4	Sequence 4, Appli
72	4	10.3	29	3	US-09-348-578-12	Sequence 12, Appl
73	4	10.3	29	3	US-09-348-578-20	Sequence 20, Appl
74	4	10.3	29	4	US-09-507-819-46	Sequence 46, Appl
75	4	10.3	29	4	US-09-092-291-4	Sequence 4, Appli
76	4	10.3	29	4	US-09-586-472-46	Sequence 46, Appl
77	4	10.3	29	4	US-09-586-472-48	Sequence 48, Appl
78	4	10.3	29	4	US-09-311-311C-12	Sequence 12, Appl
79	4	10.3	29	4	US-09-560-915-1	Sequence 1, Appli
80	4	10.3	29	4	US-08-817-441-33	Sequence 33, Appl
81	4	10.3	29	4	US-09-149-476-743	Sequence 743, App
82	4	10.3	29	4	US-09-699-684-4	Sequence 4, Appli
83	4	10.3	29	4	US-09-699-684-12	Sequence 12, Appl
84	4	10.3	29	4	US-09-699-684-20	Sequence 20, Appl
85	4	10.3	29	4	US-09-528-706-46	Sequence 46, Appl
86	4	10.3	29	4	US-09-528-706-48	Sequence 48, Appl
87	4	10.3	29	4	US-09-461-325-368	Sequence 368, App
88	4	10.3	29	4	US-09-708-906-2	Sequence 2, Appli
89	4	10.3	29	4	US-09-708-906-3	Sequence 3, Appli
90	4	10.3	29	4	US-09-708-906-4	Sequence 4, Appli
91	4	10.3	29	4	US-09-708-906-5	Sequence 5, Appli
92	4	10.3	29	4	US-09-708-906-6	Sequence 6, Appli
93	4	10.3	29	4	US-09-708-906-7	Sequence 7, Appli
94	4	10.3	29	4	US-09-708-906-8	Sequence 8, Appli
95	4	10.3	29	4	US-09-641-576-46	Sequence 46, Appl
96	4	10.3	29	5	PCT-US92-03965-12	Sequence 12, Appl
97	4	10.3	29	6	5498694-4	Patent No. 5498694
98	4	10.3	30	1	US-07-596-081A-35	Sequence 35, Appl
99	4	10.3	30	1	US-07-901-874B-11	Sequence 11, Appl
100	4	10.3	30	1	US-08-414-804-1	Sequence 1, Appli
101	4	10.3	30	1	US-08-066-325-60	Sequence 60, Appl
102	4	10.3	30	1	US-08-457-865-11	Sequence 11, Appl
103	4	10.3	30	1	US-08-451-947-40	Sequence 40, Appl
104	4	10.3	30	1	US-08-451-947-43	Sequence 43, Appl
105	4	10.3	30	2	US-08-424-826A-40	Sequence 40, Appl
106	4	10.3	30	2	US-08-424-826A-43	Sequence 43, Appl
107	4	10.3	30	2	US-08-956-047-28	Sequence 28, Appl
108	4	10.3	30	2	US-08-280-864A-9	Sequence 9, Appli
109	4	10.3	30	2	US-08-244-657-1	Sequence 1, Appli
110	4	10.3	30	2	US-08-152-721B-25	Sequence 25, Appl
111	4	10.3	30	3	US-08-928-694-40	Sequence 40, Appl
112	4	10.3	30	3	US-08-928-694-43	Sequence 43, Appl
113	4	10.3	30	3	US-08-943-173-15	Sequence 15, Appl
114	4	10.3	30	3	US-09-348-578-5	Sequence 5, Appli
115	4	10.3	30	3	US-09-348-578-13	Sequence 13, Appl
116	4	10.3	30	3	US-09-348-578-21	Sequence 21, Appl
117	4	10.3	30	3	US-08-448-489-7	Sequence 7, Appli
118	4	10.3	30	4	US-09-092-291-9	Sequence 9, Appli
119	4	10.3	30	4	US-09-185-501B-1	Sequence 1, Appli
120	4	10.3	30	4	US-09-149-476-443	Sequence 443, App
121	4	10.3	30	4	US-09-699-684-5	Sequence 5, Appli
122	4	10.3	30	4	US-09-699-684-13	Sequence 13, Appl
123	4	10.3	30	4	US-09-699-684-21	Sequence 21, Appl
124	4	10.3	30	4	US-08-450-842-40	Sequence 40, Appl
125	4	10.3	30	4	US-08-450-842-43	Sequence 43, Appl

126	4	10.3	30	4	US-09-671-317-489	Sequence 489, App
127	4	10.3	30	4	US-08-451-390-40	Sequence 40, Appl
128	4	10.3	30	4	US-08-451-390-43	Sequence 43, Appl
129	4	10.3	30	4	US-09-509-593-6	Sequence 6, Appli
130	4	10.3	30	5	PCT-US91-06950-40	Sequence 40, Appl
131	4	10.3	30	5	PCT-US91-06950-43	Sequence 43, Appli
132	4	10.3	31	1	US-07-829-462-3	Sequence 3, Appli
133	4	10.3	31	1	US-08-418-716A-3	Sequence 3, Appli
134	4	10.3	31	1	US-08-340-812-3	Sequence 3, Appli
135	4	10.3	31	1	US-08-053-131-91	Sequence 91, Appl
136	4	10.3	31	1	US-08-066-325-76	Sequence 76, Appl
137	4	10.3	31	1	US-08-066-325-77	Sequence 77, Appl
138	4	10.3	31	1	US-08-066-325-78	Sequence 78, Appl
139	4	10.3	31	1	US-08-427-001C-45	Sequence 45, Appl
140	4	10.3	31	1	US-08-645-641-91	Sequence 91, Appl
141	4	10.3	31	1	US-08-459-064B-3	Sequence 3, Appli
142	4	10.3	31	1	US-07-853-408B-91	Sequence 91, Appl
143	4	10.3	31	2	US-08-096-762-91	Sequence 91, Appl
144	4	10.3	31	2	US-08-572-951-25	Sequence 25, Appl
145	4	10.3	31	2	US-08-572-951-26	Sequence 26, Appl
146	4	10.3	31	2	US-08-460-421A-3	Sequence 3, Appli
147	4	10.3	31	2	US-08-939-002A-9	Sequence 9, Appli
148	4	10.3	31	2	US-08-723-306-20	Sequence 20, Appl
149	4	10.3	31	2	US-08-723-306-26	Sequence 26, Appl
150	4	10.3	31	2	US-08-723-306-29	Sequence 29, Appl
151	4	10.3	31	2	US-08-308-865-91	Sequence 91, Appl
152	4	10.3	31	2	US-08-428-257A-50	Sequence 50, Appl
153	4	10.3	31	3	US-08-519-385B-1	Sequence 1, Appli
154	4	10.3	31	3	US-08-444-818-146	Sequence 146, App
155	4	10.3	31	3	US-09-348-578-6	Sequence 6, Appli
156	4	10.3	31	3	US-09-348-578-14	Sequence 14, Appl
157	4	10.3	31	3	US-09-348-578-22	Sequence 22, Appl
158	4	10.3	31	3	US-09-042-353-288	Sequence 288, App
159	4	10.3	31	4	US-08-758-417A-136	Sequence 136, App
160	4	10.3	31	4	US-09-507-819-48	Sequence 48, Appl
161	4	10.3	31	4	US-08-525-539A-5	Sequence 5, Appli
162	4	10.3	31	4	US-09-227-357-398	Sequence 398, App
163	4	10.3	31	4	US-09-699-684-6	Sequence 6, Appli
164	4	10.3	31	4	US-09-699-684-14	Sequence 14, Appl
165	4	10.3	31	4	US-09-699-684-22	Sequence 22, Appl
166	4	10.3	31	4	US-09-496-118B-3	Sequence 3, Appli
167	4	10.3	31	4	US-09-205-258-383	Sequence 383, App
168	4	10.3	31	4	US-09-641-576-48	Sequence 48, Appl
169	4	10.3	31	4	US-09-019-922A-45	Sequence 45, Appl
170	4	10.3	31	5	PCT-US92-10983-91	Sequence 91, Appl
171	4	10.3	31	5	PCT-US93-00909-3	Sequence 3, Appli
172	4	10.3	31	5	PCT-US94-12550-48	Sequence 48, Appl
173	4	10.3	31	5	PCT-US96-10041-20	Sequence 20, Appl
174	4	10.3	31	5	PCT-US96-10041-26	Sequence 26, Appl
175	4	10.3	31	5	PCT-US96-10041-29	Sequence 29, Appl
176	4	10.3	31	6	5198348-5	Patent No. 5198348
177	4	10.3	31	6	5245013-18	Patent No. 5245013
178	4	10.3	32	1	US-07-662-005A-8	Sequence 8, Appli
179	4	10.3	32	1	US-07-963-290A-3	Sequence 3, Appli
180	4	10.3	32	1	US-08-145-708A-7	Sequence 7, Appli
181	4	10.3	32	1	US-08-158-189-31	Sequence 31, Appl
182	4	10.3	32	1	US-08-468-700-38	Sequence 38, Appl

183	4	10.3	32	2	US-08-468-220-38	Sequence 38, Appl
184	4	10.3	32	2	US-08-491-204A-15	Sequence 15, Appl
185	4	10.3	32	2	US-08-468-698-38	Sequence 38, Appl
186	4	10.3	32	2	US-08-373-190-29	Sequence 29, Appl
187	4	10.3	32	2	US-08-078-311-25	Sequence 25, Appl
188	4	10.3	32	2	US-08-704-706A-38	Sequence 38, Appl
189	4	10.3	32	2	US-08-438-190A-29	Sequence 29, Appl
190	4	10.3	32	2	US-08-331-454-7	Sequence 7, Appli
191	4	10.3	32	2	US-08-460-402-25	Sequence 25, Appl
192	4	10.3	32	3	US-08-350-215-29	Sequence 29, Appl
193	4	10.3	32	3	US-09-287-145A-29	Sequence 29, Appl
194	4	10.3	32	3	US-08-641-873-19	Sequence 19, Appl
195	4	10.3	32	3	US-09-348-578-7	Sequence 7, Appli
196	4	10.3	32	3	US-09-348-578-15	Sequence 15, Appl
197	4	10.3	32	3	US-09-348-578-23	Sequence 23, Appl
198	4	10.3	32	3	US-08-985-659-39	Sequence 39, Appl
199	4	10.3	32	3	US-08-194-664A-38	Sequence 38, Appl
200	4	10.3	32	4	US-09-556-111-29	Sequence 29, Appl
201	4	10.3	32	4	US-09-352-078-7	Sequence 7, Appli
202	4	10.3	32	4	US-09-227-357-181	Sequence 181, App
203	4	10.3	32	4	US-09-699-684-7	Sequence 7, Appli
204	4	10.3	32	4	US-09-699-684-15	Sequence 15, Appl
205	4	10.3	32	4	US-09-699-684-23	Sequence 23, Appl
206	4	10.3	32	4	US-09-030-619-193	Sequence 193, App
207	4	10.3	32	4	US-09-030-619-194	Sequence 194, App
208	4	10.3	32	4	US-09-625-972-30	Sequence 30, Appl
209	4	10.3	32	4	US-09-625-972-31	Sequence 31, Appl
210	4	10.3	32	5	PCT-US94-01553A-38	Sequence 38, Appl
211	4	10.3	32	5	PCT-US95-10426-38	Sequence 38, Appl
212	4	10.3	33	1	US-08-038-343A-3	Sequence 3, Appli
213	4	10.3	33	1	US-08-158-189-26	Sequence 26, Appl
214	4	10.3	33	1	US-08-290-448A-5	Sequence 5, Appli
215	4	10.3	33	1	US-08-290-448A-6	Sequence 6, Appli
216	4	10.3	33	1	US-08-290-448A-5	Sequence 5, Appli
217	4	10.3	33	1	US-08-290-448A-6	Sequence 6, Appli
218	4	10.3	33	1	US-08-460-874A-28	Sequence 28, Appl
219	4	10.3	33	1	US-08-175-069A-5	Sequence 5, Appli
220	4	10.3	33	1	US-08-175-069A-6	Sequence 6, Appli
221	4	10.3	33	2	US-08-572-951-5	Sequence 5, Appli
222	4	10.3	33	2	US-08-491-204A-10	Sequence 10, Appl
223	4	10.3	33	2	US-08-388-883B-28	Sequence 28, Appl
224	4	10.3	33	3	US-08-462-211A-28	Sequence 28, Appl
225	4	10.3	33	3	US-09-433-428D-1	Sequence 1, Appli
226	4	10.3	33	3	US-09-433-428D-3	Sequence 3, Appli
227	4	10.3	33	3	US-09-433-428D-4	Sequence 4, Appli
228	4	10.3	33	3	US-09-433-428D-5	Sequence 5, Appli
229	4	10.3	33	3	US-09-433-428D-6	Sequence 6, Appli
230	4	10.3	33	3	US-09-433-428D-7	Sequence 7, Appli
231	4	10.3	33	3	US-09-433-428D-8	Sequence 8, Appli
232	4	10.3	33	3	US-09-433-428D-9	Sequence 9, Appli
233	4	10.3	33	3	US-09-433-428D-10	Sequence 10, Appli
234	4	10.3	33	3	US-09-433-428D-11	Sequence 11, Appli
235	4	10.3	33	3	US-09-433-428D-12	Sequence 12, Appli
236	4	10.3	33	3	US-09-433-428D-14	Sequence 14, Appli
237	4	10.3	33	3	US-09-433-428D-15	Sequence 15, Appli
238	4	10.3	33	3	US-09-433-428D-16	Sequence 16, Appli
239	4	10.3	33	3	US-09-433-428D-18	Sequence 18, Appli

240	4	10.3	33	3	US-09-433-428D-19	Sequence 19, Appl
241	4	10.3	33	3	US-09-433-428D-21	Sequence 21, Appl
242	4	10.3	33	3	US-09-433-428D-22	Sequence 22, Appl
243	4	10.3	33	3	US-09-433-428D-25	Sequence 25, Appl
244	4	10.3	33	3	US-09-433-428D-27	Sequence 27, Appl
245	4	10.3	33	3	US-09-433-428D-28	Sequence 28, Appl
246	4	10.3	33	3	US-09-433-428D-29	Sequence 29, Appl
247	4	10.3	33	3	US-09-433-428D-30	Sequence 30, Appl
248	4	10.3	33	3	US-09-348-578-8	Sequence 8, Appli
249	4	10.3	33	3	US-09-348-578-16	Sequence 16, Appl
250	4	10.3	33	3	US-09-348-578-24	Sequence 24, Appl
251	4	10.3	33	3	US-08-205-697A-36	Sequence 36, Appl
252	4	10.3	33	3	US-07-741-453A-12	Sequence 12, Appl
253	4	10.3	33	3	US-07-741-453A-13	Sequence 13, Appl
254	4	10.3	33	3	US-08-702-525-36	Sequence 36, Appl
255	4	10.3	33	4	US-08-461-939B-5	Sequence 5, Appli
256	4	10.3	33	4	US-08-461-939B-6	Sequence 6, Appli
257	4	10.3	33	4	US-08-464-000-5	Sequence 5, Appli
258	4	10.3	33	4	US-08-464-000-6	Sequence 6, Appli
259	4	10.3	33	4	US-09-390-425-16	Sequence 16, Appl
260	4	10.3	33	4	US-09-566-906-16	Sequence 16, Appl
261	4	10.3	33	4	US-09-586-563C-9	Sequence 9, Appli
262	4	10.3	33	4	US-09-586-562C-9	Sequence 9, Appli
263	4	10.3	33	4	US-09-257-179-69	Sequence 69, Appl
264	4	10.3	33	4	US-09-699-684-8	Sequence 8, Appli
265	4	10.3	33	4	US-09-699-684-16	Sequence 16, Appl
266	4	10.3	33	4	US-09-699-684-24	Sequence 24, Appl
267	4	10.3	33	4	US-09-030-619-186	Sequence 186, App
268	4	10.3	33	4	US-09-030-619-192	Sequence 192, App
269	4	10.3	33	5	PCT-US95-02576-36	Sequence 36, Appl
270	4	10.3	33	6	5498694-6	Patent No. 5498694
271	4	10.3	34	1	US-07-596-081A-15	Sequence 15, Appl
272	4	10.3	34	1	US-08-163-181-1	Sequence 1, Appli
273	4	10.3	34	1	US-08-465-161-1	Sequence 1, Appli
274	4	10.3	34	1	US-08-190-802A-262	Sequence 262, App
275	4	10.3	34	1	US-08-449-500-65	Sequence 65, Appl
276	4	10.3	34	1	US-08-449-317A-65	Sequence 65, Appl
277	4	10.3	34	2	US-08-477-022-65	Sequence 65, Appl
278	4	10.3	34	2	US-08-449-447-65	Sequence 65, Appl
279	4	10.3	34	2	US-08-184-328-65	Sequence 65, Appl
280	4	10.3	34	2	US-08-521-097-65	Sequence 65, Appl
281	4	10.3	34	2	US-08-934-741A-3	Sequence 3, Appli
282	4	10.3	34	3	US-08-630-172-41	Sequence 41, Appl
283	4	10.3	34	3	US-09-348-578-9	Sequence 9, Appli
284	4	10.3	34	3	US-09-348-578-17	Sequence 17, Appl
285	4	10.3	34	3	US-09-348-578-25	Sequence 25, Appl
286	4	10.3	34	3	US-08-477-346-262	Sequence 262, App
287	4	10.3	34	3	US-09-375-419-41	Sequence 41, Appl
288	4	10.3	34	4	US-08-473-089-262	Sequence 262, App
289	4	10.3	34	4	US-09-000-094-28	Sequence 28, Appl
290	4	10.3	34	4	US-09-301-978C-29	Sequence 29, Appl
291	4	10.3	34	4	US-08-487-072A-262	Sequence 262, App
292	4	10.3	34	4	US-09-699-684-9	Sequence 9, Appli
293	4	10.3	34	4	US-09-699-684-17	Sequence 17, Appl
294	4	10.3	34	4	US-09-699-684-25	Sequence 25, Appl
295	4	10.3	35	1	US-08-560-727-1	Sequence 1, Appli
296	4	10.3	35	1	US-08-487-890A-53	Sequence 53, Appl

297	4	10.3	35	2	US-08-142-551B-76	Sequence 76, Appl
298	4	10.3	35	2	US-08-337-127-10	Sequence 10, Appl
299	4	10.3	35	2	US-08-478-435-53	Sequence 53, Appl
300	4	10.3	35	2	US-08-337-483-53	Sequence 53, Appl
301	4	10.3	35	2	US-08-478-373-53	Sequence 53, Appl
302	4	10.3	35	2	US-08-766-858A-41	Sequence 41, Appl
303	4	10.3	35	2	US-08-574-959A-20	Sequence 20, Appl
304	4	10.3	35	2	US-08-938-975-3	Sequence 3, Appli
305	4	10.3	35	3	US-08-474-671-53	Sequence 53, Appl
306	4	10.3	35	3	US-08-483-577A-53	Sequence 53, Appl
307	4	10.3	35	3	US-09-433-428D-64	Sequence 64, Appl
308	4	10.3	35	3	US-09-348-578-18	Sequence 18, Appl
309	4	10.3	35	3	US-09-348-578-26	Sequence 26, Appl
310	4	10.3	35	3	US-08-196-748-1	Sequence 1, Appli
311	4	10.3	35	3	US-08-196-748-2	Sequence 2, Appli
312	4	10.3	35	3	US-08-196-748-3	Sequence 3, Appli
313	4	10.3	35	3	US-09-248-588-26	Sequence 26, Appl
314	4	10.3	35	3	US-09-082-279B-458	Sequence 458, App
315	4	10.3	35	3	US-09-082-279B-459	Sequence 459, App
316	4	10.3	35	3	US-09-082-279B-460	Sequence 460, App
317	4	10.3	35	3	US-09-082-279B-461	Sequence 461, App
318	4	10.3	35	3	US-09-082-279B-462	Sequence 462, App
319	4	10.3	35	3	US-09-082-279B-463	Sequence 463, App
320	4	10.3	35	3	US-09-082-279B-464	Sequence 464, App
321	4	10.3	35	3	US-09-082-279B-465	Sequence 465, App
322	4	10.3	35	3	US-09-082-279B-466	Sequence 466, App
323	4	10.3	35	3	US-09-082-279B-467	Sequence 467, App
324	4	10.3	35	3	US-09-082-279B-468	Sequence 468, App
325	4	10.3	35	3	US-09-082-279B-469	Sequence 469, App
326	4	10.3	35	3	US-09-082-279B-470	Sequence 470, App
327	4	10.3	35	3	US-09-082-279B-471	Sequence 471, App
328	4	10.3	35	3	US-09-082-279B-472	Sequence 472, App
329	4	10.3	35	3	US-09-082-279B-473	Sequence 473, App
330	4	10.3	35	3	US-09-082-279B-474	Sequence 474, App
331	4	10.3	35	3	US-09-082-279B-475	Sequence 475, App
332	4	10.3	35	3	US-09-082-279B-476	Sequence 476, App
333	4	10.3	35	3	US-09-082-279B-477	Sequence 477, App
334	4	10.3	35	3	US-09-082-279B-478	Sequence 478, App
335	4	10.3	35	3	US-09-082-279B-479	Sequence 479, App
336	4	10.3	35	3	US-09-082-279B-480	Sequence 480, App
337	4	10.3	35	3	US-09-082-279B-481	Sequence 481, App
338	4	10.3	35	3	US-09-082-279B-482	Sequence 482, App
339	4	10.3	35	3	US-09-082-279B-483	Sequence 483, App
340	4	10.3	35	3	US-09-082-279B-518	Sequence 518, App
341	4	10.3	35	3	US-09-082-279B-519	Sequence 519, App
342	4	10.3	35	3	US-09-082-279B-717	Sequence 717, App
343	4	10.3	35	3	US-09-082-279B-1220	Sequence 1220, Ap
344	4	10.3	35	3	US-09-082-279B-1221	Sequence 1221, Ap
345	4	10.3	35	3	US-09-082-279B-1222	Sequence 1222, Ap
346	4	10.3	35	3	US-08-897-438-53	Sequence 53, Appl
347	4	10.3	35	3	US-09-357-014-20	Sequence 20, Appl
348	4	10.3	35	4	US-08-749-066A-6	Sequence 6, Appli
349	4	10.3	35	4	US-09-260-846-10	Sequence 10, Appl
350	4	10.3	35	4	US-08-474-349A-484	Sequence 484, App
351	4	10.3	35	4	US-08-474-349A-485	Sequence 485, App
352	4	10.3	35	4	US-08-474-349A-495	Sequence 495, App
353	4	10.3	35	4	US-08-474-349A-496	Sequence 496, App

354	4	10.3	35	4	US-08-474-349A-497	Sequence 497, App
355	4	10.3	35	4	US-08-474-349A-498	Sequence 498, App
356	4	10.3	35	4	US-08-474-349A-499	Sequence 499, App
357	4	10.3	35	4	US-08-474-349A-500	Sequence 500, App
358	4	10.3	35	4	US-08-474-349A-501	Sequence 501, App
359	4	10.3	35	4	US-08-474-349A-502	Sequence 502, App
360	4	10.3	35	4	US-08-474-349A-503	Sequence 503, App
361	4	10.3	35	4	US-08-474-349A-504	Sequence 504, App
362	4	10.3	35	4	US-08-474-349A-505	Sequence 505, App
363	4	10.3	35	4	US-08-474-349A-506	Sequence 506, App
364	4	10.3	35	4	US-08-474-349A-507	Sequence 507, App
365	4	10.3	35	4	US-08-474-349A-508	Sequence 508, App
366	4	10.3	35	4	US-08-474-349A-509	Sequence 509, App
367	4	10.3	35	4	US-08-474-349A-510	Sequence 510, App
368	4	10.3	35	4	US-08-474-349A-511	Sequence 511, App
369	4	10.3	35	4	US-08-474-349A-512	Sequence 512, App
370	4	10.3	35	4	US-08-474-349A-513	Sequence 513, App
371	4	10.3	35	4	US-08-474-349A-514	Sequence 514, App
372	4	10.3	35	4	US-08-474-349A-515	Sequence 515, App
373	4	10.3	35	4	US-08-474-349A-516	Sequence 516, App
374	4	10.3	35	4	US-08-474-349A-517	Sequence 517, App
375	4	10.3	35	4	US-09-315-304B-458	Sequence 458, App
376	4	10.3	35	4	US-09-315-304B-459	Sequence 459, App
377	4	10.3	35	4	US-09-315-304B-460	Sequence 460, App
378	4	10.3	35	4	US-09-315-304B-461	Sequence 461, App
379	4	10.3	35	4	US-09-315-304B-462	Sequence 462, App
380	4	10.3	35	4	US-09-315-304B-463	Sequence 463, App
381	4	10.3	35	4	US-09-315-304B-464	Sequence 464, App
382	4	10.3	35	4	US-09-315-304B-465	Sequence 465, App
383	4	10.3	35	4	US-09-315-304B-466	Sequence 466, App
384	4	10.3	35	4	US-09-315-304B-467	Sequence 467, App
385	4	10.3	35	4	US-09-315-304B-468	Sequence 468, App
386	4	10.3	35	4	US-09-315-304B-469	Sequence 469, App
387	4	10.3	35	4	US-09-315-304B-470	Sequence 470, App
388	4	10.3	35	4	US-09-315-304B-471	Sequence 471, App
389	4	10.3	35	4	US-09-315-304B-472	Sequence 472, App
390	4	10.3	35	4	US-09-315-304B-473	Sequence 473, App
391	4	10.3	35	4	US-09-315-304B-474	Sequence 474, App
392	4	10.3	35	4	US-09-315-304B-475	Sequence 475, App
393	4	10.3	35	4	US-09-315-304B-476	Sequence 476, App
394	4	10.3	35	4	US-09-315-304B-477	Sequence 477, App
395	4	10.3	35	4	US-09-315-304B-478	Sequence 478, App
396	4	10.3	35	4	US-09-315-304B-479	Sequence 479, App
397	4	10.3	35	4	US-09-315-304B-480	Sequence 480, App
398	4	10.3	35	4	US-09-315-304B-481	Sequence 481, App
399	4	10.3	35	4	US-09-315-304B-482	Sequence 482, App
400	4	10.3	35	4	US-09-315-304B-483	Sequence 483, App
401	4	10.3	35	4	US-09-315-304B-518	Sequence 518, App
402	4	10.3	35	4	US-09-315-304B-519	Sequence 519, App
403	4	10.3	35	4	US-09-315-304B-717	Sequence 717, App
404	4	10.3	35	4	US-09-315-304B-1220	Sequence 1220, Ap
405	4	10.3	35	4	US-09-315-304B-1221	Sequence 1221, Ap
406	4	10.3	35	4	US-09-315-304B-1222	Sequence 1222, Ap
407	4	10.3	35	4	US-08-637-654-53	Sequence 53, Appl
408	4	10.3	35	4	US-08-649-518-53	Sequence 53, Appl
409	4	10.3	35	4	US-09-321-399-3	Sequence 3, Appli
410	4	10.3	35	4	US-08-817-441-101	Sequence 101, App

411	4	10.3	35	4	US-09-699-684-18	Sequence 18, Appl
412	4	10.3	35	4	US-09-699-684-26	Sequence 26, Appl
413	4	10.3	35	4	US-09-645-470-33	Sequence 33, Appl
414	4	10.3	35	4	US-09-322-379-3	Sequence 3, Appli
415	4	10.3	35	4	US-09-834-784-458	Sequence 458, App
416	4	10.3	35	4	US-09-834-784-459	Sequence 459, App
417	4	10.3	35	4	US-09-834-784-460	Sequence 460, App
418	4	10.3	35	4	US-09-834-784-461	Sequence 461, App
419	4	10.3	35	4	US-09-834-784-462	Sequence 462, App
420	4	10.3	35	4	US-09-834-784-463	Sequence 463, App
421	4	10.3	35	4	US-09-834-784-464	Sequence 464, App
422	4	10.3	35	4	US-09-834-784-465	Sequence 465, App
423	4	10.3	35	4	US-09-834-784-466	Sequence 466, App
424	4	10.3	35	4	US-09-834-784-467	Sequence 467, App
425	4	10.3	35	4	US-09-834-784-468	Sequence 468, App
426	4	10.3	35	4	US-09-834-784-469	Sequence 469, App
427	4	10.3	35	4	US-09-834-784-470	Sequence 470, App
428	4	10.3	35	4	US-09-834-784-471	Sequence 471, App
429	4	10.3	35	4	US-09-834-784-472	Sequence 472, App
430	4	10.3	35	4	US-09-834-784-473	Sequence 473, App
431	4	10.3	35	4	US-09-834-784-474	Sequence 474, App
432	4	10.3	35	4	US-09-834-784-475	Sequence 475, App
433	4	10.3	35	4	US-09-834-784-476	Sequence 476, App
434	4	10.3	35	4	US-09-834-784-477	Sequence 477, App
435	4	10.3	35	4	US-09-834-784-478	Sequence 478, App
436	4	10.3	35	4	US-09-834-784-479	Sequence 479, App
437	4	10.3	35	4	US-09-834-784-480	Sequence 480, App
438	4	10.3	35	4	US-09-834-784-481	Sequence 481, App
439	4	10.3	35	4	US-09-834-784-482	Sequence 482, App
440	4	10.3	35	4	US-09-834-784-483	Sequence 483, App
441	4	10.3	35	4	US-09-834-784-518	Sequence 518, App
442	4	10.3	35	4	US-09-834-784-519	Sequence 519, App
443	4	10.3	35	4	US-09-834-784-717	Sequence 717, App
444	4	10.3	35	4	US-09-834-784-1220	Sequence 1220, Ap
445	4	10.3	35	4	US-09-834-784-1221	Sequence 1221, Ap
446	4	10.3	35	4	US-09-834-784-1222	Sequence 1222, Ap
447	4	10.3	35	6	5171673-7	Patent No. 5171673
448	4	10.3	36	1	US-08-162-102C-34	Sequence 34, Appl
449	4	10.3	36	3	US-09-348-578-27	Sequence 27, Appl
450	4	10.3	36	3	US-09-082-279B-541	Sequence 541, App
451	4	10.3	36	3	US-09-082-279B-542	Sequence 542, App
452	4	10.3	36	3	US-09-082-279B-751	Sequence 751, App
453	4	10.3	36	3	US-09-082-279B-1034	Sequence 1034, Ap
454	4	10.3	36	4	US-09-315-304B-541	Sequence 541, App
455	4	10.3	36	4	US-09-315-304B-542	Sequence 542, App
456	4	10.3	36	4	US-09-315-304B-751	Sequence 751, App
457	4	10.3	36	4	US-09-315-304B-1034	Sequence 1034, Ap
458	4	10.3	36	4	US-09-000-094-30	Sequence 30, Appl
459	4	10.3	36	4	US-09-699-684-27	Sequence 27, Appl
460	4	10.3	36	4	US-09-834-784-541	Sequence 541, App
461	4	10.3	36	4	US-09-834-784-542	Sequence 542, App
462	4	10.3	36	4	US-09-834-784-751	Sequence 751, App
463	4	10.3	36	4	US-09-834-784-1034	Sequence 1034, Ap
464	4	10.3	37	1	US-07-649-591B-1	Sequence 1, Appli
465	4	10.3	37	1	US-08-277-540-1	Sequence 1, Appli
466	4	10.3	37	1	US-08-190-802A-225	Sequence 225, App
467	4	10.3	37	1	US-08-430-787A-1	Sequence 1, Appli

468	4	10.3	37	1	US-08-252-966B-5	Sequence 5, Appl
469	4	10.3	37	2	US-08-631-328-45	Sequence 45, Appl
470	4	10.3	37	2	US-08-631-328-47	Sequence 47, Appl
471	4	10.3	37	2	US-08-631-328-48	Sequence 48, Appl
472	4	10.3	37	3	US-08-919-597-240	Sequence 240, App
473	4	10.3	37	3	US-08-919-597-241	Sequence 241, App
474	4	10.3	37	3	US-08-919-597-251	Sequence 251, App
475	4	10.3	37	3	US-08-919-597-252	Sequence 252, App
476	4	10.3	37	3	US-08-919-597-253	Sequence 253, App
477	4	10.3	37	3	US-08-919-597-254	Sequence 254, App
478					-08-919-597-255	Sequence 255, App
479	4	10.3	37	3	US-08-919-597-256	Sequence 256, App
480	4	10.3	37	3	US-08-919-597-257	Sequence 257, App
481	4	10.3	37	3	US-08-919-597-258	Sequence 258, App
482	4	10.3	37	3	US-08-919-597-259	Sequence 259, App
483	4	10.3	37	3	US-08-919-597-260	Sequence 260, App
484	4	10.3	37	3	US-08-919-597-261	Sequence 261, App
485	4	10.3	37	3	US-08-919-597-262	Sequence 262, App
486	4	10.3	37	3	US-08-919-597-263	Sequence 263, App
487	4	10.3	37	3	US-08-919-597-264	Sequence 264, App
488	4	10.3	37	3	US-08-919-597-265	Sequence 265, App
489	4	10.3	37	3	US-08-919-597-266	Sequence 266, App
490	4	10.3	37	3	US-08-919-597-267	Sequence 267, App
491	4	10.3	37	3	US-08-919-597-268	Sequence 268, App
492	4	10.3	37	3	US-08-919-597-269	Sequence 269, App
493	4	10.3	37	3	US-08-919-597-270	Sequence 270, App
494	4	10.3	37	3	US-08-919-597-271	Sequence 271, App
495	4	10.3	37	3	US-08-919-597-272	Sequence 272, App
496	4	10.3	37	3	US-08-919-597-273	Sequence 273, App
497	4	10.3	37	3	US-09-346-860-15	Sequence 15, Appl
498	4	10.3	37	3	US-08-477-346-225	Sequence 225, App
499	4	10.3	37	4	US-08-473-089-225	Sequence 225, App
500	4	10.3	37	4	US-08-817-441-84	Sequence 84, Appl
501	4	10.3	37	4	US-08-817-441-86	Sequence 86, Appl
502	4	10.3	37	4	US-08-817-441-90	Sequence 90, Appl
503	4	10.3	37	4	US-08-817-441-94	Sequence 94, Appl
504	4	10.3	37	4	US-08-487-072A-225	Sequence 225, App
505	4	10.3	37	4	US-09-461-325-265	Sequence 265, App
506	4	10.3	37	4	US-09-023-905A-23	Sequence 23, Appl
507	4	10.3	37	4	US-08-470-896-240	Sequence 240, App
508	4	10.3	37	4	US-08-470-896-241	Sequence 241, App
509	4	10.3	37	4	US-08-470-896-251	Sequence 251, App
510	4	10.3	37	4	US-08-470-896-252	Sequence 252, App
511	4	10.3	37	4	US-08-470-896-253	Sequence 253, App
512	4	10.3	37	4	US-08-470-896-254	Sequence 254, App
513	4	10.3	37	4	US-08-470-896-255	Sequence 255, App
514	4	10.3	37	4	US-08-470-896-256	Sequence 256, App
515	4	10.3	37	4	US-08-470-896-257	Sequence 257, App
516	4	10.3	37	4	US-08-470-896-258	Sequence 258, App
517	4	10.3	37	4	US-08-470-896-259	Sequence 259, App
518	4	10.3	37	4	US-08-470-896-260	Sequence 260, App
519	4	10.3	37	4	US-08-470-896-261	Sequence 261, App
520	4	10.3	37	4	US-08-470-896-262	Sequence 262, App
521	4	10.3	37	4	US-08-470-896-263	Sequence 263, App
522	4	10.3	37	4	US-08-470-896-264	Sequence 264, App
523	4	10.3	37	4	US-08-470-896-265	Sequence 265, App
524	4	10.3	37	4	US-08-470-896-266	Sequence 266, App

525	4	10.3	37	4	US-08-470-896-267	Sequence 267, App
526	4	10.3	37	4	US-08-470-896-268	Sequence 268, App
527	4	10.3	37	4	US-08-470-896-269	Sequence 269, App
528	4	10.3	37	4	US-08-470-896-270	Sequence 270, App
529	4	10.3	37	4	US-08-470-896-271	Sequence 271, App
530	4	10.3	37	4	US-08-470-896-272	Sequence 272, App
531	4	10.3	37	4	US-08-470-896-273	Sequence 273, App
532	4	10.3	37	4	US-09-735-685-15	Sequence 15, Appl
533	4	10.3	37	5	PCT-US93-06829-1	Sequence 1, Appli
534	4	10.3	38	1	US-08-451-472-11	Sequence 11, Appl
535	4	10.3	38	1	US-08-451-472-40	Sequence 40, Appl
536	4	10.3	38	1	US-08-451-472-56	Sequence 56, Appl
537	4	10.3	38	2	US-08-723-306-21	Sequence 21, Appl
538	4	10.3	38	2	US-08-723-306-23	Sequence 23, Appl
539	4	10.3	38	2	US-08-662-227-36	Sequence 36, Appl
540	4	10.3	38	2	US-08-530-290-17	Sequence 17, Appl
541	4	10.3	38	3	US-08-460-576-5	Sequence 5, Appli
542	4	10.3	38	3	US-08-974-549A-211	Sequence 211, App
543	4	10.3	38	3	US-09-172-841-39	Sequence 39, Appl
544	4	10.3	38	3	US-09-082-279B-83	Sequence 83, Appl
545	4	10.3	38	4	US-09-017-947-36	Sequence 36, Appl
546	4	10.3	38	4	US-09-315-304B-83	Sequence 83, Appl
547	4	10.3	38	4	US-09-201-227A-31	Sequence 31, Appl
548	4	10.3	38	4	US-09-390-134B-34	Sequence 34, Appl
549	4	10.3	38	4	US-09-834-784-83	Sequence 83, Appl
550	4	10.3	38	4	US-08-951-621-39	Sequence 39, Appl
551	4	10.3	38	5	PCT-US96-10041-21	Sequence 21, Appl
552	4	10.3	38	5	PCT-US96-10041-23	Sequence 23, Appl
553	4	10.3	38	6	5196194-5	Patent No. 5196194
554	4	10.3	39	2	US-08-350-260A-52	Sequence 52, Appl
555	4	10.3	39	3	US-08-792-832A-55	Sequence 55, Appl
556	4	10.3	39	3	US-08-905-223-459	Sequence 459, App
557	4	10.3	39	3	US-09-238-303-13	Sequence 13, Appl
558	4	10.3	39	3	US-09-220-528-48	Sequence 48, Appl
559	4	10.3	39	3	US-08-988-856B-12	Sequence 12, Appl
560	4	10.3	39	4	US-09-227-357-384	Sequence 384, App
561	4	10.3	39	4	US-09-227-357-672	Sequence 672, App
562	4	10.3	39	4	US-09-315-304B-1457	Sequence 1457, Ap
563	4	10.3	39	4	US-09-315-304B-1529	Sequence 1529, Ap
564	4	10.3	39	4	US-09-104-337A-52	Sequence 52, Appl
565	4	10.3	39	4	US-09-205-258-354	Sequence 354, App
566	4	10.3	39	4	US-09-205-258-559	Sequence 559, App
567	4	10.3	39	4	US-09-205-258-1206	Sequence 1206, Ap
568	4	10.3	39	4	US-08-733-622C-35	Sequence 35, Appl
569	4	10.3	39	4	US-09-634-238-314	Sequence 314, App
570	4	10.3	39	4	US-09-946-239-13	Sequence 13, Appl
571	4	10.3	40	1	US-07-901-874B-5	Sequence 5, Appli
572	4	10.3	40	1	US-07-946-054-2	Sequence 2, Appli
573	4	10.3	40	1	US-08-457-865-5	Sequence 5, Appli
574	4	10.3	40	1	US-08-262-037-8	Sequence 8, Appli
575	4	10.3	40	1	US-08-262-037-119	Sequence 119, App
576	4	10.3	40	1	US-08-262-037-120	Sequence 120, App
577	4	10.3	40	2	US-08-939-002A-2	Sequence 2, Appli
578	4	10.3	40	2	US-08-557-309B-27	Sequence 27, Appl
579	4	10.3	40	3	US-08-689-421-1	Sequence 1, Appli
580	4	10.3	40	3	US-08-894-699-38	Sequence 38, Appl
581	4	10.3	40	3	US-08-894-699-41	Sequence 41, Appl

582	4	10.3	40	3	US-08-894-699-42	Sequence 42, Appl
583	4	10.3	40	3	US-08-834-306-27	Sequence 27, Appl
584	4	10.3	40	3	US-09-068-650-5	Sequence 5, Appl
585	4	10.3	40	3	US-09-389-528-1	Sequence 1, Appl
586	4	10.3	40	3	US-08-981-189B-8	Sequence 8, Appl
587	4	10.3	40	3	US-08-993-674A-27	Sequence 27, Appl
588	4	10.3	40	3	US-09-181-827A-1	Sequence 1, Appl
589	4	10.3	40	3	US-09-444-410-38	Sequence 38, Appl
590	4	10.3	40	3	US-09-444-410-41	Sequence 41, Appl
591	4	10.3	40	3	US-09-444-410-42	Sequence 42, Appl
592	4	10.3	40	3	US-08-988-856B-13	Sequence 13, Appl
593	4	10.3	40	4	US-09-400-716-10	Sequence 10, Appl
594	4	10.3	40	4	US-09-400-716-11	Sequence 11, Appl
595	4	10.3	40	4	US-09-256-976-27	Sequence 27, Appl
596	4	10.3	40	4	US-09-149-476-535	Sequence 535, App
597	4	10.3	40	4	US-08-706-054A-11	Sequence 11, Appl
598	4	10.3	40	4	US-09-461-325-312	Sequence 312, App
599	4	10.3	40	4	US-09-284-768A-34	Sequence 34, Appl
600	4	10.3	40	4	US-09-690-454-140	Sequence 140, App
601	4	10.3	40	4	US-09-060-299-14	Sequence 14, Appl
602	4	10.3	40	4	US-09-402-923A-14	Sequence 14, Appl
603	4	10.3	40	4	US-09-313-299-11	Sequence 11, Appl
604	4	10.3	40	5	PCT-US93-08638-2	Sequence 2, Appl
605	4	10.3	40	6	5196194-7	Patent No. 5196194
606	3	7.7	28	1	US-07-620-410-2	Sequence 2, Appl
607	3	7.7	28	1	US-07-602-847C-20	Sequence 20, Appl
608	3	7.7	28	1	US-07-690-300B-1	Sequence 1, Appl
609	3	7.7	28	1	US-07-690-300B-23	Sequence 23, Appl
610	3	7.7	28	1	US-07-690-300B-24	Sequence 24, Appl
611	3	7.7	28	1	US-07-690-300B-25	Sequence 25, Appl
612	3	7.7	28	1	US-07-690-300B-26	Sequence 26, Appl
613	3	7.7	28	1	US-07-690-300B-29	Sequence 29, Appl
614	3	7.7	28	1	US-07-690-300B-30	Sequence 30, Appl
615	3	7.7	28	1	US-07-690-300B-31	Sequence 31, Appl
616	3	7.7	28	1	US-07-690-300B-32	Sequence 32, Appl
617	3	7.7	28	1	US-07-690-300B-33	Sequence 33, Appl
618	3	7.7	28	1	US-07-690-300B-34	Sequence 34, Appl
619	3	7.7	28	1	US-07-690-300B-35	Sequence 35, Appl
620	3	7.7	28	1	US-07-690-300B-36	Sequence 36, Appl
621	3	7.7	28	1	US-07-690-300B-37	Sequence 37, Appl
622	3	7.7	28	1	US-07-690-300B-38	Sequence 38, Appl
623	3	7.7	28	1	US-07-690-300B-39	Sequence 39, Appl
624	3	7.7	28	1	US-07-690-300B-40	Sequence 40, Appl
625	3	7.7	28	1	US-07-690-300B-41	Sequence 41, Appl
626	3	7.7	28	1	US-07-690-300B-42	Sequence 42, Appl
627	3	7.7	28	1	US-07-690-300B-43	Sequence 43, Appl
628	3	7.7	28	1	US-07-690-300B-45	Sequence 45, Appl
629	3	7.7	28	1	US-07-690-300B-46	Sequence 46, Appl
630	3	7.7	28	1	US-07-690-300B-47	Sequence 47, Appl
631	3	7.7	28	1	US-07-690-300B-48	Sequence 48, Appl
632	3	7.7	28	1	US-07-690-300B-49	Sequence 49, Appl
633	3	7.7	28	1	US-07-690-300B-50	Sequence 50, Appl
634	3	7.7	28	1	US-07-690-300B-51	Sequence 51, Appl
635	3	7.7	28	1	US-07-690-300B-52	Sequence 52, Appl
636	3	7.7	28	1	US-07-690-300B-53	Sequence 53, Appl
637	3	7.7	28	1	US-07-690-300B-54	Sequence 54, Appl
638	3	7.7	28	1	US-07-690-300B-55	Sequence 55, Appl

639	3	7.7	28	1	US-07-690-300B-56	Sequence 56, Appl
640	3	7.7	28	1	US-07-690-300B-63	Sequence 63, Appl
641	3	7.7	28	1	US-07-690-300B-64	Sequence 64, Appl
642	3	7.7	28	1	US-07-690-300B-68	Sequence 68, Appl
643	3	7.7	28	1	US-07-690-300B-71	Sequence 71, Appl
644	3	7.7	28	1	US-07-690-300B-78	Sequence 78, Appl
645	3	7.7	28	1	US-07-690-300B-79	Sequence 79, Appl
646	3	7.7	28	1	US-07-690-300B-82	Sequence 82, Appl
647	3	7.7	28	1	US-07-690-300B-88	Sequence 88, Appl
648	3	7.7	28	1	US-07-690-300B-91	Sequence 91, Appl
649	3	7.7	28	1	US-07-690-300B-93	Sequence 93, Appl
650	3	7.7	28	1	US-07-787-148C-3	Sequence 3, Appli
651	3	7.7	28	1	US-07-778-233B-10	Sequence 10, Appl
652	3	7.7	28	1	US-07-778-233B-12	Sequence 12, Appl
653	3	7.7	28	1	US-07-778-233B-56	Sequence 56, Appl
654	3	7.7	28	1	US-07-676-987A-1	Sequence 1, Appli
655	3	7.7	28	1	US-07-676-987A-2	Sequence 2, Appli
656	3	7.7	28	1	US-07-833-468-1	Sequence 1, Appli
657	3	7.7	28	1	US-08-055-917-19	Sequence 19, Appl
658	3	7.7	28	1	US-07-963-321-10	Sequence 10, Appl
659	3	7.7	28	1	US-07-963-321-12	Sequence 12, Appl
660	3	7.7	28	1	US-07-963-321-56	Sequence 56, Appl
661	3	7.7	28	1	US-08-095-068-19	Sequence 19, Appl
662	3	7.7	28	1	US-07-868-906-1	Sequence 1, Appli
663	3	7.7	28	1	US-08-201-092-1	Sequence 1, Appli
664	3	7.7	28	1	US-08-201-092-2	Sequence 2, Appli
665	3	7.7	28	1	US-07-901-874B-17	Sequence 17, Appl
666	3	7.7	28	1	US-08-255-558B-9	Sequence 9, Appli
667	3	7.7	28	1	US-08-255-558B-10	Sequence 10, Appl
668	3	7.7	28	1	US-08-255-558B-12	Sequence 12, Appl
669	3	7.7	28	1	US-08-140-721A-19	Sequence 19, Appl
670	3	7.7	28	1	US-07-924-054-11	Sequence 11, Appl
671	3	7.7	28	1	US-08-290-641-10	Sequence 10, Appl
672	3	7.7	28	1	US-08-290-641-12	Sequence 12, Appl
673	3	7.7	28	1	US-08-290-641-56	Sequence 56, Appl
674	3	7.7	28	1	US-08-243-082-1	Sequence 1, Appli
675	3	7.7	28	1	US-08-246-572-4	Sequence 4, Appli
676	3	7.7	28	1	US-08-246-572-5	Sequence 5, Appli
677	3	7.7	28	1	US-08-164-151-22	Sequence 22, Appl
678	3	7.7	28	1	US-08-361-443-1	Sequence 1, Appli
679	3	7.7	28	1	US-08-276-213-4	Sequence 4, Appli
680	3	7.7	28	1	US-07-949-797B-1	Sequence 1, Appli
681	3	7.7	28	1	US-08-182-175A-1	Sequence 1, Appli
682	3	7.7	28	1	US-08-457-605-4	Sequence 4, Appli
683	3	7.7	28	1	US-08-194-591-1	Sequence 1, Appli
684	3	7.7	28	1	US-08-194-591-2	Sequence 2, Appli
685	3	7.7	28	1	US-08-257-446-6	Sequence 6, Appli
686	3	7.7	28	1	US-07-977-630-39	Sequence 39, Appl
687	3	7.7	28	1	US-07-977-630-44	Sequence 44, Appl
688	3	7.7	28	1	US-07-977-630-45	Sequence 45, Appl
689	3	7.7	28	1	US-07-977-630-46	Sequence 46, Appl
690	3	7.7	28	1	US-07-977-630-48	Sequence 48, Appl
691	3	7.7	28	1	US-07-977-630-52	Sequence 52, Appl
692	3	7.7	28	1	US-07-977-630-53	Sequence 53, Appl
693	3	7.7	28	1	US-08-350-884-36	Sequence 36, Appl
694	3	7.7	28	1	US-08-288-681A-1	Sequence 1, Appli
695	3	7.7	28	1	US-08-366-591-12	Sequence 12, Appl

696	3	7.7	28	1	US-08-179-632-10	Sequence 10, Appl
697	3	7.7	28	1	US-07-776-272-26	Sequence 26, Appl
698	3	7.7	28	1	US-08-056-200-13	Sequence 13, Appl
699	3	7.7	28	1	US-08-056-200-14	Sequence 14, Appl
700	3	7.7	28	1	US-08-340-428B-12	Sequence 12, Appl
701	3	7.7	28	1	US-08-486-057B-11	Sequence 11, Appl
702	3	7.7	28	1	US-08-440-391-9	Sequence 9, Appli
703	3	7.7	28	1	US-08-440-391-30	Sequence 30, Appl
704	3	7.7	28	1	US-08-133-011-8	Sequence 8, Appli
705	3	7.7	28	1	US-08-053-131-98	Sequence 98, Appl
706	3	7.7	28	1	US-08-473-334B-7	Sequence 7, Appli
707	3	7.7	28	1	US-08-473-334B-10	Sequence 10, Appl
708	3	7.7	28	1	US-08-473-334B-11	Sequence 11, Appl
709	3	7.7	28	1	US-08-473-334B-12	Sequence 12, Appl
710	3	7.7	28	1	US-08-473-334B-13	Sequence 13, Appl
711	3	7.7	28	1	US-08-473-334B-14	Sequence 14, Appl
712	3	7.7	28	1	US-08-473-334B-15	Sequence 15, Appl
713	3	7.7	28	1	US-08-473-334B-16	Sequence 16, Appl
714	3	7.7	28	1	US-08-473-334B-19	Sequence 19, Appl
715	3	7.7	28	1	US-08-473-334B-20	Sequence 20, Appl
716	3	7.7	28	1	US-08-473-334B-21	Sequence 21, Appl
717	3	7.7	28	1	US-08-473-334B-22	Sequence 22, Appl
718	3	7.7	28	1	US-08-473-334B-23	Sequence 23, Appl
719	3	7.7	28	1	US-08-473-334B-24	Sequence 24, Appl
720	3	7.7	28	1	US-08-331-394-21	Sequence 21, Appl
721	3	7.7	28	1	US-08-308-729-1	Sequence 1, Appli
722	3	7.7	28	1	US-08-308-729-21	Sequence 21, Appl
723	3	7.7	28	1	US-08-308-729-22	Sequence 22, Appl
724	3	7.7	28	1	US-08-308-729-23	Sequence 23, Appl
725	3	7.7	28	1	US-08-308-729-24	Sequence 24, Appl
726	3	7.7	28	1	US-08-308-729-25	Sequence 25, Appl
727	3	7.7	28	1	US-08-308-729-26	Sequence 26, Appl
728	3	7.7	28	1	US-08-308-729-59	Sequence 59, Appl
729	3	7.7	28	1	US-08-308-729-61	Sequence 61, Appl
730	3	7.7	28	1	US-08-308-729-62	Sequence 62, Appl
731	3	7.7	28	1	US-08-308-729-64	Sequence 64, Appl
732	3	7.7	28	1	US-08-457-865-17	Sequence 17, Appl
733	3	7.7	28	1	US-08-062-472B-39	Sequence 39, Appl
734	3	7.7	28	1	US-08-062-472B-40	Sequence 40, Appl
735	3	7.7	28	1	US-08-250-858-21	Sequence 21, Appl
736	3	7.7	28	1	US-08-709-173-36	Sequence 36, Appl
737	3	7.7	28	1	US-08-507-313-6	Sequence 6, Appli
738	3	7.7	28	1	US-08-786-748A-1	Sequence 1, Appli
739	3	7.7	28	1	US-08-786-748A-14	Sequence 14, Appl
740	3	7.7	28	1	US-08-786-748A-15	Sequence 15, Appl
741	3	7.7	28	1	US-08-786-748A-16	Sequence 16, Appl
742	3	7.7	28	1	US-08-786-748A-17	Sequence 17, Appl
743	3	7.7	28	1	US-08-786-748A-18	Sequence 18, Appl
744	3	7.7	28	1	US-08-786-748A-24	Sequence 24, Appl
745	3	7.7	28	1	US-08-786-748A-25	Sequence 25, Appl
746	3	7.7	28	1	US-08-786-748A-26	Sequence 26, Appl
747	3	7.7	28	1	US-08-786-748A-27	Sequence 27, Appl
748	3	7.7	28	1	US-08-786-748A-161	Sequence 161, App
749	3	7.7	28	1	US-08-786-748A-162	Sequence 162, App
750	3	7.7	28	1	US-08-786-748A-163	Sequence 163, App
751	3	7.7	28	1	US-08-786-748A-164	Sequence 164, App
752	3	7.7	28	1	US-08-786-748A-165	Sequence 165, App

753	3	7.7	28	1	US-08-786-748A-169	Sequence 169, Appl
754	3	7.7	28	1	US-08-440-174A-10	Sequence 10, Appl
755	3	7.7	28	1	US-08-645-641-98	Sequence 98, Appl
756	3	7.7	28	1	US-08-171-701A-1	Sequence 1, Appl
757	3	7.7	28	1	US-08-171-701A-2	Sequence 2, Appl
758	3	7.7	28	1	US-08-261-660A-17	Sequence 17, Appl
759	3	7.7	28	1	US-08-548-540-10	Sequence 10, Appl
760	3	7.7	28	1	US-08-548-540-12	Sequence 12, Appl
761	3	7.7	28	1	US-08-548-540-56	Sequence 56, Appl
762	3	7.7	28	1	US-08-741-678-1	Sequence 1, Appl
763	m43	7.7	28	1	US-08-446-915-21	Sequence 21, Appl
764	3	7.7	28	1	US-08-442-029-9	Sequence 9, Appl
765	3	7.7	28	1	US-08-446-692-3	Sequence 3, Appl
766	3	7.7	28	1	US-08-446-692-38	Sequence 38, Appl
767	3	7.7	28	1	US-08-322-730A-8	Sequence 8, Appl
768	3	7.7	28	1	US-08-387-874-8	Sequence 8, Appl
769	3	7.7	28	1	US-08-519-180-2	Sequence 2, Appl
770	3	7.7	28	1	US-08-427-072-8	Sequence 8, Appl
771	3	7.7	28	1	US-08-427-072-11	Sequence 11, Appl
772	3	7.7	28	1	US-07-853-408B-98	Sequence 98, Appl
773	3	7.7	28	1	US-08-449-500-81	Sequences 81, Appl
774	3	7.7	28	1	US-08-420-235B-13	Sequence 13, Appl
775	3	7.7	28	1	US-08-258-852-4	Sequence 4, Appl
776	3	7.7	28	1	US-08-449-317A-81	Sequence 81, Appl
777	3	7.7	28	2	US-08-096-762-98	Sequence 98, Appl
778	3	7.7	28	2	US-08-477-022-81	Sequence 81, Appl
779	3	7.7	28	2	US-08-449-447-81	Sequence 81, Appl
780	3	7.7	28	2	US-08-660-789-8	Sequence 8, Appl
781	3	7.7	28	2	US-08-488-351A-3	Sequence 3, Appl
782	3	7.7	28	2	US-08-488-351A-38	Sequence 38, Appl
783	3	7.7	28	2	US-08-414-424-1	Sequence 1, Appl
784	1875Xa	7.7	28	2	US-08-776-815B-2	Sequences 25, Appl
785	3	7.7	28	2	US-08-388-883B-3	Sequence 3, Appl
786	3	7.7	28	2	US-08-392-816-4	Sequence 4, Appl
787	3	7.7	28	2	US-08-908-597A-9	Sequence 9, Appl
788	3	7.7	28	2	US-08-908-597A-30	Sequence 30, Appl
789	3	7.7	28	2	US-07-785-565A-19	Sequence 19, Appl
790	3	7.7	28	2	US-08-454-549-6	Sequence 6, Appl
791	3	7.7	28	2	US-08-679-405-8	Sequence 8, Appl
792	3	7.7	28	2	US-08-596-387B-105	Sequence 105, App
793	3	7.7	28	2	US-08-744-139-21	Sequence 21, Appl
794	3	7.7	28	2	US-08-184-328-81	Sequence 81, Appl
795	3	7.7	28	2	US-08-637-759B-489	Sequence 489, App
796	3	7.7	28	2	US-08-308-865-98	Sequence 98, Appl
797	3	7.7	28	2	US-08-488-161-48	Sequence 48, Appl
798	3	7.7	28	2	US-08-488-161-49	Sequence 49, Appl
799	3	7.7	28	2	US-08-709-177-36	Sequence 36, Appl
800	3	7.7	28	2	US-08-103-170-32	Sequence 32, Appl
801	3	7.7	28	2	US-08-789-588-11	Sequence 11, Appl
802	3	7.7	28	2	US-07-814-220-36	Sequence 36, Appl
803	3	7.7	28	2	US-08-620-151-4	Sequence 4, Appl
804	3	7.7	28	2	US-08-620-151-74	Sequence 74, Appl
805	3	7.7	28	2	US-08-620-151-129	Sequence 129, App
806	3	7.7	28	2	US-07-812-421-36	Sequence 36, Appl
807	3	7.7	28	2	US-08-821-619-10	Sequence 10, Appl
808	3	7.7	28	2	US-08-932-682-1	Sequence 1, Appl
809	3	7.7	28	2	US-08-932-682-14	Sequence 14, Appl

810	3	7.7	28	2	US-08-932-682-15	Sequence 15, Appl
811	3	7.7	28	2	US-08-932-682-16	Sequence 16, Appl
812	3	7.7	28	2	US-08-932-682-17	Sequence 17, Appl
813	3	7.7	28	2	US-08-932-682-18	Sequence 18, Appl
814	3	7.7	28	2	US-08-932-682-24	Sequence 24, Appl
815	3	7.7	28	2	US-08-932-682-25	Sequence 25, Appl
816	3	7.7	28	2	US-08-932-682-26	Sequence 26, Appl
817	3	7.7	28	2	US-08-932-682-27	Sequence 27, Appl
818	3	7.7	28	2	US-08-932-682-161	Sequence 161, App
819	3	7.7	28	2	US-08-932-682-162	Sequence 162, App
820	3	7.7	28	2	US-08-932-682-163	Sequence 163, App
821	3	7.7	28	2	US-08-932-682-164	Sequence 164, App
822	3	7.7	28	2	US-08-932-682-165	Sequence 165, App
823	3	7.7	28	2	US-08-932-682-169	Sequence 169, App
824	3	7.7	28	2	US-08-383-619-8	Sequence 8, Appli
825	3	7.7	28	2	US-08-706-741B-36	Sequence 36, Appl
826	3	7.7	28	2	US-08-726-306A-131	Sequence 131, App
827	3	7.7	28	2	US-08-726-306A-132	Sequence 132, App
828	3	7.7	28	2	US-08-800-644-13	Sequence 13, Appl
829	3	7.7	28	2	US-08-800-644-14	Sequence 14, Appl
830	3	7.7	28	2	US-08-574-959A-19	Sequence 19, Appl
831	3	7.7	28	2	US-08-842-799-8	Sequence 8, Appli
832	3	7.7	28	2	US-08-413-708B-1	Sequence 1, Appli
833	3	7.7	28	2	US-08-413-708B-2	Sequence 2, Appli
834	3	7.7	28	2	US-08-563-892A-5	Sequence 5, Appli
835	3	7.7	28	2	US-08-521-097-81	Sequence 81, Appl
836	3	7.7	28	2	US-08-691-814B-73	Sequence 73, Appl
837	3	7.7	28	2	US-08-310-912A-6	Sequence 6, Appli
838	3	7.7	28	2	US-09-072-323-6	Sequence 6, Appli
839	3	7.7	28	2	US-08-846-762-62	Sequence 62, Appl
840	3	7.7	28	2	US-08-818-253-22	Sequence 22, Appl
841	3	7.7	28	2	US-08-818-253-37	Sequence 37, Appl
842	3	7.7	28	2	US-08-897-624-1	Sequence 1, Appli
843	3	7.7	28	2	US-08-897-624-2	Sequence 2, Appli
844	3	7.7	28	2	US-08-924-695A-36	Sequence 36, Appl
845	3	7.7	28	3	US-09-045-632-85	Sequence 85, Appl
846	3	7.7	28	3	US-08-938-548B-4	Sequence 4, Appli
847	3	7.7	28	3	US-08-938-548B-9	Sequence 9, Appli
848	3	7.7	28	3	US-08-938-548B-12	Sequence 12, Appl
849	3	7.7	28	3	US-08-454-552-6	Sequence 6, Appli
850	3	7.7	28	3	US-08-930-845-1	Sequence 1, Appli
851	3	7.7	28	3	US-08-486-099-84	Sequence 84, Appl
852	3	7.7	28	3	US-08-486-099-86	Sequence 86, Appl
853	3	7.7	28	3	US-08-486-099-87	Sequence 87, Appl
854	3	7.7	28	3	US-08-486-099-131	Sequence 131, App
855	3	7.7	28	3	US-08-486-099-133	Sequence 133, App
856	3	7.7	28	3	US-08-486-099-161	Sequence 161, App
857	3	7.7	28	3	US-08-433-522A-38	Sequence 38, Appl
858	3	7.7	28	3	US-08-848-580-10	Sequence 10, Appl
859	3	7.7	28	3	US-08-916-043-1	Sequence 1, Appli
860	3	7.7	28	3	US-09-273-685-48	Sequence 48, Appl
861	3	7.7	28	3	US-09-273-685-49	Sequence 49, Appl
862	3	7.7	28	3	US-08-871-355A-489	Sequence 489, App
863	3	7.7	28	3	US-08-360-107A-94	Sequence 94, Appl
864	3	7.7	28	3	US-08-360-107A-96	Sequence 96, Appl
865	3	7.7	28	3	US-08-360-107A-97	Sequence 97, Appl
866	3	7.7	28	3	US-08-484-223B-84	Sequence 84, Appl

867	3	7.7	28	3	US-08-484-223B-86	Sequence 86, Appl
868	3	7.7	28	3	US-08-484-223B-87	Sequence 87, Appl
869	3	7.7	28	3	US-08-484-223B-131	Sequence 131, App
870	3	7.7	28	3	US-08-484-223B-133	Sequence 133, App
871	3	7.7	28	3	US-08-484-223B-161	Sequence 161, App
872	3	7.7	28	3	US-09-100-414B-37	Sequence 37, Appl
873	3	7.7	28	3	US-09-100-414B-74	Sequence 74, Appl
874	3	7.7	28	3	US-08-952-568-1	Sequence 1, Appli
875	3	7.7	28	3	US-08-952-568-2	Sequence 2, Appli
876	3	7.7	28	3	US-08-952-568-3	Sequence 3, Appli
877	3	7.7	28	3	US-08-952-568-4	Sequence 4, Appli
878	3	7.7	28	3	US-08-952-568-5	Sequence 5, Appli
879	3	7.7	28	3	US-08-952-568-6	Sequence 6, Appli
880	3	7.7	28	3	US-08-952-568-7	Sequence 7, Appli
881	3	7.7	28	3	US-08-952-568-9	Sequence 9, Appli
882	3	7.7	28	3	US-08-952-568-10	Sequence 10, Appl
883	3	7.7	28	3	US-08-952-568-11	Sequence 11, Appl
884	3	7.7	28	3	US-08-952-568-12	Sequence 12, Appl
885	3	7.7	28	3	US-08-952-568-13	Sequence 13, Appl
886	3	7.7	28	3	US-08-952-568-14	Sequence 14, Appl
887	3	7.7	28	3	US-09-170-754B-4	Sequence 4, Appli
888	3	7.7	28	3	US-08-948-782-5	Sequence 5, Appli
889	3	7.7	28	3	US-08-812-586-17	Sequence 17, Appl
890	3	7.7	28	3	US-08-919-597-84	Sequence 84, Appl
891	3	7.7	28	3	US-08-919-597-86	Sequence 86, Appl
892	3	7.7	28	3	US-08-919-597-87	Sequence 87, Appl
893	3	7.7	28	3	US-08-919-597-131	Sequence 131, App
894	3	7.7	28	3	US-08-919-597-133	Sequence 133, App
895	3	7.7	28	3	US-08-919-597-161	Sequence 161, App
896	3	7.7	28	3	US-08-984-277-7	Sequence 7, Appli
897	3	7.7	28	3	US-08-475-668A-84	Sequence 84, Appl
898	3	7.7	28	3	US-08-475-668A-86	Sequence 86, Appl
899	3	7.7	28	3	US-08-475-668A-87	Sequence 87, Appl
900	3	7.7	28	3	US-08-475-668A-131	Sequence 131, App
901	3	7.7	28	3	US-08-475-668A-133	Sequence 133, App
902	3	7.7	28	3	US-08-475-668A-161	Sequence 161, App
903	3	7.7	28	3	US-09-192-048-21	Sequence 21, Appl
904	3	7.7	28	3	US-08-485-551A-84	Sequence 84, Appl
905	3	7.7	28	3	US-08-485-551A-86	Sequence 86, Appl
906	3	7.7	28	3	US-08-485-551A-87	Sequence 87, Appl
907	3	7.7	28	3	US-08-485-551A-131	Sequence 131, App
908	3	7.7	28	3	US-08-485-551A-133	Sequence 133, App
909	3	7.7	28	3	US-08-485-551A-161	Sequence 161, App
910	3	7.7	28	3	US-09-135-166-38	Sequence 38, Appl
911	3	7.7	28	3	US-08-467-023-81	Sequence 81, Appl
912	3	7.7	28	3	US-08-467-023-82	Sequence 82, Appl
913	3	7.7	28	3	US-08-467-023-85	Sequence 85, Appl
914	3	7.7	28	3	US-08-467-023-88	Sequence 88, Appl
915	3	7.7	28	3	US-08-467-023-217	Sequence 217, App
916	3	7.7	28	3	US-08-467-023-218	Sequence 218, App
917	3	7.7	28	3	US-08-467-023-219	Sequence 219, App
918	3	7.7	28	3	US-08-467-023-223	Sequence 223, App
919	3	7.7	28	3	US-08-471-913A-84	Sequence 84, Appl
920	3	7.7	28	3	US-08-471-913A-86	Sequence 86, Appl
921	3	7.7	28	3	US-08-471-913A-87	Sequence 87, Appl
922	3	7.7	28	3	US-08-471-913A-131	Sequence 131, App
923	3	7.7	28	3	US-08-471-913A-133	Sequence 133, App

924	3	7.7	28	3	US-08-471-913A-161	Sequence 161, App
925	3	7.7	28	3	US-08-851-843A-115	Sequence 115, App
926	3	7.7	28	3	US-08-147-592A-14	Sequence 14, Appl
927	3	7.7	28	3	US-08-147-592A-15	Sequence 15, Appl
928	3	7.7	28	3	US-08-641-873-8	Sequence 8, Appli
929	3	7.7	28	3	US-08-893-749-2	Sequence 2, Appli
930	3	7.7	28	3	US-08-893-749-3	Sequence 3, Appli
931	3	7.7	28	3	US-08-893-749-32	Sequence 32, Appl
932	3	7.7	28	3	US-08-841-089-6	Sequence 6, Appli
933	3	7.7	28	3	US-08-822-324-23	Sequence 23, Appl
934	3	7.7	28	3	US-09-074-114-8	Sequence 8, Appli
935	3	7.7	28	3	US-09-433-428D-62	Sequence 62, Appl
936	3	7.7	28	3	US-08-793-624-13	Sequence 13, Appl
937	3	7.7	28	3	US-08-796-899-30	Sequence 30, Appl
938	3	7.7	28	3	US-09-040-485-5	Sequence 5, Appli
939	3	7.7	28	3	US-08-974-549A-235	Sequence 235, App
940	3	7.7	28	3	US-08-819-286-18	Sequence 18, Appl
941	3	7.7	28	3	US-08-817-811-13	Sequence 13, Appl
942	3	7.7	28	3	US-08-817-811-14	Sequence 14, Appl
943	3	7.7	28	3	US-08-817-811-15	Sequence 15, Appl
944	3	7.7	28	3	US-08-817-811-16	Sequence 16, Appl
945	3	7.7	28	3	US-08-817-811-17	Sequence 17, Appl
946	3	7.7	28	3	US-08-817-811-67	Sequence 67, Appl
947	3	7.7	28	3	US-08-818-252-22	Sequence 22, Appl
948	3	7.7	28	3	US-08-818-252-37	Sequence 37, Appl
949	3	7.7	28	3	US-08-363-558-1	Sequence 1, Appli
950	3	7.7	28	3	US-09-253-396A-221	Sequence 221, App
951	3	7.7	28	3	US-09-253-396A-229	Sequence 229, App
952	3	7.7	28	3	US-09-236-385A-9	Sequence 9, Appli
953	3	7.7	28	3	US-09-236-385A-30	Sequence 30, Appl
954	3	7.7	28	3	US-08-905-223-357	Sequence 357, App
955	3	7.7	28	3	US-08-957-001B-25	Sequence 25, Appl
956	3	7.7	28	3	US-08-485-264A-84	Sequence 84, Appl
957	3	7.7	28	3	US-08-485-264A-86	Sequence 86, Appl
958	3	7.7	28	3	US-08-485-264A-87	Sequence 87, Appl
959	3	7.7	28	3	US-08-485-264A-131	Sequence 131, App
960	3	7.7	28	3	US-08-485-264A-133	Sequence 133, App
961	3	7.7	28	3	US-08-485-264A-161	Sequence 161, App
962	3	7.7	28	3	US-08-485-264A-211	Sequence 211, App
963	3	7.7	28	3	US-09-303-323-37	Sequence 37, Appl
964	3	7.7	28	3	US-09-303-323-74	Sequence 74, Appl
965	3	7.7	28	3	US-09-177-249-73	Sequence 73, Appl
966	3	7.7	28	3	US-09-248-588-42	Sequence 42, Appl
967	3	7.7	28	3	US-08-907-739-8	Sequence 8, Appli
968	3	7.7	28	3	US-09-041-886-50	Sequence 50, Appl
969	3	7.7	28	3	US-09-041-886-56	Sequence 56, Appl
970	3	7.7	28	3	US-09-127-680-2	Sequence 2, Appli
971	3	7.7	28	3	US-08-995-369-1	Sequence 1, Appli
972	3	7.7	28	3	US-09-171-654-1	Sequence 1, Appli
973	3	7.7	28	3	US-09-496-301-25	Sequence 25, Appl
974	3	7.7	28	3	US-09-482-612-5	Sequence 5, Appli
975	3	7.7	28	3	US-09-082-279B-8	Sequence 8, Appli
976	3	7.7	28	3	US-09-082-279B-12	Sequence 12, Appl
977	3	7.7	28	3	US-09-082-279B-14	Sequence 14, Appl
978	3	7.7	28	3	US-09-082-279B-50	Sequence 50, Appl
979	3	7.7	28	3	US-09-082-279B-54	Sequence 54, Appl
980	3	7.7	28	3	US-09-082-279B-63	Sequence 63, Appl

981	3	7.7	28	3	US-09-082-279B-68	Sequence 68, Appl
982	3	7.7	28	3	US-09-082-279B-75	Sequence 75, Appl
983	3	7.7	28	3	US-09-082-279B-82	Sequence 82, Appl
984	3	7.7	28	3	US-09-082-279B-231	Sequence 231, App
985	3	7.7	28	3	US-09-082-279B-673	Sequence 673, App
986	3	7.7	28	3	US-09-082-279B-674	Sequence 674, App
987	3	7.7	28	3	US-09-082-279B-675	Sequence 675, App
988	3	7.7	28	3	US-09-082-279B-676	Sequence 676, App
989	3	7.7	28	3	US-09-082-279B-836	Sequence 836, App
990	3	7.7	28	3	US-09-082-279B-891	Sequence 891, App
991	3	7.7	28	3	US-09-082-279B-908	Sequence 908, App
992	3	7.7	28	3	US-09-082-279B-909	Sequence 909, App
993	3	7.7	28	3	US-09-082-279B-910	Sequence 910, App
994	3	7.7	28	3	US-09-082-279B-911	Sequence 911, App
995	3	7.7	28	3	US-09-082-279B-914	Sequence 914, App
996	3	7.7	28	3	US-09-082-279B-915	Sequence 915, App
997	3	7.7	28	3	US-09-082-279B-958	Sequence 958, App
998	3	7.7	28	3	US-09-082-279B-982	Sequence 982, App
999	3	7.7	28	3	US-09-082-279B-1029	Sequence 1029, Ap
1000	3	7.7	28	4	US-09-442-989-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-09-041-886-53

; Sequence 53, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-886-53

Query Match 15.4%; Score 6; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAALE 21
| | | | |
Db 21 LLAALE 26

RESULT 2

US-08-817-441-7

; Sequence 7, Application US/08817441
; Patent No. 6399294
; GENERAL INFORMATION:
; APPLICANT: CHARNEAU, PIERRE
; APPLICANT: CLAVEL, FRANCOISE
; APPLICANT: BORMAN, ANDREW
; APPLICANT: QUILLENT, CAROLINE
; APPLICANT: GUETARD, DENISE
; APPLICANT: MONTAGNIER, LUC
; APPLICANT: DONJON DE SAINT-MARTIN, JACQUELINE
; APPLICANT: COHEN, JAQUES
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
; TITLE OF INVENTION: SUBTYPE) ANTIGENS
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,441
; FILING DATE: 11-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR 95/01391
; FILING DATE: 20-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9412554
; FILING DATE: 20-OCT-1994
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 9502526
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03260.6005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-817-441-7

Query Match 15.4%; Score 6; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
|||||||
Db 1 RARLLA 6

RESULT 3
US-08-894-699-36
; Sequence 36, Application US/08894699
; Patent No. 6030769
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,699
; FILING DATE: 01-DEC-1997

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/00294
; FILING DATE: 26-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-894-699-36

Query Match 15.4%; Score 6; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
 |||||||
Db 4 RARLLA 9

RESULT 4

US-08-894-699-37

; Sequence 37, Application US/08894699

; Patent No. 6030769

; GENERAL INFORMATION:

; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF

; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,699
; FILING DATE: 01-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/00294
; FILING DATE: 26-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-894-699-37

Query Match 15.4%; Score 6; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
|||||
Db 4 RARLLA 9

RESULT 5
US-08-894-699-39
; Sequence 39, Application US/08894699
; Patent No. 6030769
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA

; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,699
; FILING DATE: 01-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/00294
; FILING DATE: 26-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-894-699-39

Query Match 15.4%; Score 6; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
| | | | |
Db 4 RARLLA 9

RESULT 6

US-08-894-699-40

; Sequence 40, Application US/08894699
; Patent No. 6030769
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,699
; FILING DATE: 01-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/00294
; FILING DATE: 26-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-894-699-40

Query Match 15.4%; Score 6; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
| | | | |
Db 4 RARLLA 9

RESULT 7
US-08-894-699-68
; Sequence 68, Application US/08894699
; Patent No. 6030769
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,699
; FILING DATE: 01-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/00294
; FILING DATE: 26-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-894-699-68

Query Match 15.4%; Score 6; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
Db 4 RARLLA 9

RESULT 8
US-09-444-410-36
; Sequence 36, Application US/09444410
; Patent No. 6270975
; GENERAL INFORMATION:

; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/444,410
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/894,699
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-444-410-36

Query Match 15.4%; Score 6; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
| | | | |
Db 4 RARLLA 9

RESULT 9
US-09-444-410-37
; Sequence 37, Application US/09444410
; Patent No. 6270975
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/444,410
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/894,699
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-444-410-37

Query Match 15.4%; Score 6; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18

|||||

Db 4 RARLLA 9

RESULT 10

US-09-444-410-39

; Sequence 39, Application US/09444410
; Patent No. 6270975
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/444,410
; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/894,699
; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.

; REGISTRATION NUMBER: 24,614

; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 39:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 40 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-444-410-39

Query Match 15.4%; Score 6; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 RARLLA 18
| | | | |
Db 4 RARLLA 9

RESULT 11

US-09-444-410-40

; Sequence 40, Application US/09444410

; Patent No. 6270975

; GENERAL INFORMATION:

; APPLICANT: SIMON, FRANCOIS

; APPLICANT: SARAGOSTI, SENTOB

; APPLICANT: LOUSSERT-AJAKA, IBITISSAM

; APPLICANT: LY, THOAI-DUONG

; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

; TITLE OF INVENTION: VIRUSES, AND USES THEREOF

; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 SOUTH JEFFERSON5Xe S HIGHWAY, FOURTH

ho n

; STREET: FLOOR

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/444,410

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/894,699

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 95/02236

; FILING DATE: 27-FEB-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.

; REGISTRATION NUMBER: 24,614

; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 40 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-444-410-40

Query Match 15.4%; Score 6; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
|||||
Db 4 RARLLA 9

RESULT 12
US-09-444-410-68
; Sequence 68, Application US/09444410
; Patent No. 6270975
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/444,410
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/894,699
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-444-410-68

Query Match 15.4%; Score 6; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
|||||||
Db 4 RARLLA 9

RESULT 13

US-09-041-886-37

; Sequence 37, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-886-37

Query Match 12.8%; Score 5; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
| | | | |
Db 21 LLAAL 25

RESULT 14
US-09-041-886-38

; Sequence 38, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-886-38

Query Match 12.8%; Score 5; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLAAL 20
 |||||
Db 21 LLAAL 25

RESULT 15
US-09-041-886-39
; Sequence 39, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-886-39

Query Match 12.8%; Score 5; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLAAL 20
 |||||
Db 21 LLAAL 25

RESULT 16

US-09-041-886-40
; Sequence 40, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-041-886-40

Query Match 12.8%; Score 5; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLAAL 20
|||
Db 21 LLAAL 25

RESULT 17
US-09-041-886-54
; Sequence 54, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence

; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-886-54

Query Match 12.8%; Score 5; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
| ||||
Db 21 LLAAL 25

RESULT 18
US-09-205-258-614
; Sequence 614, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 614
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-205-258-614

Query Match 12.8%; Score 5; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DAAFR 11
| | | |
Db 13 DAAFR 17

RESULT 19

US-08-786-284A-3

; Sequence 3, Application US/08786284A
; Patent No. 6273598
; GENERAL INFORMATION:
; APPLICANT: KECK, PETER
; APPLICANT: GRIFFITH, DIANA L
; APPLICANT: CARLSON, WILLIAM D
; APPLICANT: RUEGER, DAVID C
; APPLICANT: SAMPATH, KUBER T
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCING
; TITLE OF INVENTION: MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
; ADDRESSEE: INC.
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/786,284A
; FILING DATE:
; CLASSIFICATION: 364
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-0992
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..32
; OTHER INFORMATION: /product= "PEPTIDE H-1"
US-08-786-284A-3

Query Match 12.8%; Score 5; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 LNSYM 30
|||||
Db 5 LNSYM 9

RESULT 20
US-08-704-856C-3
; Sequence 3, Application US/08704856C
; Patent No. 6042832
; GENERAL INFORMATION:
; APPLICANT: Koprowski, Hilary
; APPLICANT: Yusibov, Vidadi
; APPLICANT: Hooper, Douglas, C.
; APPLICANT: Modelska, Anna
; TITLE OF INVENTION: Polypeptides Fused with Plant Virus
; TITLE OF INVENTION: Coat Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allan H. Fried & Associates
; STREET: 1525 Locust Street, 15th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Corel WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,856C
; FILING DATE: 28-Aug-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fried, Allan H.
; REGISTRATION NUMBER: 31,253
; REFERENCE/DOCKET NUMBER: T19-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 732-7090
; TELEFAX: (215) 732-7090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; HYPOTHETICAL: N

US-08-704-856C-3

Query Match 12.8%; Score 5; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ALADD 7
|||
Db 29 ALADD 33

RESULT 21

US-09-242-881-3

; Sequence 3, Application US/09242881

; Patent No. 6448070

; GENERAL INFORMATION:

; APPLICANT: Koprowski, Hilary
Yusibov, Vidadi
Hooper, Douglas, C.
Modelska, Anna

; TITLE OF INVENTION: Polypeptides Fused with Plant Virus
Coat Proteins

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Allan H. Fried & Associates
STREET: 1525 Locust Street, 15th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Corel WordPerfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/242,881
; FILING DATE: 25-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,856
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fried, Allan H.
; REGISTRATION NUMBER: 31,253
; REFERENCE/DOCKET NUMBER: T19-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 732-7090
; TELEFAX: (215) 732-7090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; HYPOTHETICAL: N
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-242-881-3

Query Match 12.8%; Score 5; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ALADD 7
|||||
Db 29 ALADD 33

RESULT 22
5514590-5
; Patent No. 5514590
; APPLICANT: GARVIN, ROBERT T.;MALEK, LAWRENCE T.;JAMES, ERIC
; TITLE OF INVENTION: EXPRESSION SYSTEM COMPRISING DNA
; ENCODING THE SIGNAL PEPTIDE OF PROTEASE B FROM STREPTOMYCES
; GRISEUS
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/203,644
; FILING DATE: 01-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 66,938
; FILING DATE: 25-MAY-1993
; APPLICATION NUMBER: 844,937
; FILING DATE: 04-MAR-1992
; APPLICATION NUMBER: 221,346
; FILING DATE: 18-JUL-1988
; APPLICATION NUMBER: 795,331
; FILING DATE: 06-NOV-1985
; SEQ ID NO:5:
; LENGTH: 38
5514590-5

Query Match 12.8%; Score 5; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 ARLLA 18
|||||
Db 16 ARLLA 20

RESULT 23

US-09-406-045-11

; Sequence 11, Application US/09406045
; Patent No. 6451994
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 23413, A NOVEL HUMAN UBIQUITIN
; FILE REFERENCE: 5800-50
; CURRENT APPLICATION NUMBER: US/09/406,045
; CURRENT FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ProDom consensus sequence

US-09-406-045-11

Query Match 12.8%; Score 5; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 LERRH 24
|||||
Db 15 LERRH 19

RESULT 24

US-07-690-300B-44

; Sequence 44, Application US/07690300B
; Patent No. 5234907
; GENERAL INFORMATION:
; APPLICANT: Bolin, David R.
; TITLE OF INVENTION: Synthetic Vasoactive Intestinal Peptide
; TITLE OF INVENTION: Analogs
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/690,300B
; FILING DATE: 19910424
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/374,503
; FILING DATE: 30-JUN-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Pokras, Bruce A.
; REGISTRATION NUMBER: 32,748
; REFERENCE/DOCKET NUMBER: 8480
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-5801
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 17
; OTHER INFORMATION: /note= "Xaa=Nle"
US-07-690-300B-44

Query Match 10.3%; Score 4; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DAAF 10
|||
Db 3 DAAF 6

RESULT 25

US-07-789-344A-11

; Sequence 11, Application US/07789344A
; Patent No. 5318897
; GENERAL INFORMATION:
; APPLICANT: Sudhir, Paul
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND ANTIBODY
; TITLE OF INVENTION: COMPONENTS ELICITED TO A POLYPEPTIDE ANTIGEN
; TITLE OF INVENTION: GROUND STATE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o Barry Evans
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,344A
; FILING DATE: 08-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Barry
; REGISTRATION NUMBER: 22,802
; REFERENCE/DOCKET NUMBER: 370068-3500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-07-789-344A-11

Query Match 10.3%; Score 4; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 WLNS 28
|||
Db 22 WLNS 25

RESULT 26
US-07-728-221B-3
; Sequence 3, Application US/07728221B
; Patent No. 5340920
; GENERAL INFORMATION:
; APPLICANT: Matsuo, Hisayuki
; APPLICANT: Kangawa, Kenji
; APPLICANT: Minamino, Naoto
; TITLE OF INVENTION: NOVEL HYSIOLOGICALLY ACTIVE PORCINE
; TITLE OF INVENTION: PEPTIDE (CNP-53)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: ELEVENTH FLOOR, 1615 1 STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/728,221B
; FILING DATE: 19910712
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/9437/91817/KIK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 671 4627 CUSH
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-728-221B-3

Query Match 10.3%; Score 4; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ARLL 17
|||
Db 10 ARLL 13

RESULT 27
US-08-276-852-13
; Sequence 13, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal

US-08-276-852-13

Query Match 10.3%; Score 4; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAA 19
||||
Db 14 LLAA 17

RESULT 28

US-08-664-449-37

; Sequence 37, Application US/08664449

; Patent No. 5766905

; GENERAL INFORMATION:

; APPLICANT: Studier, F. W.

; APPLICANT: Rosenberg, Alan H.

; TITLE OF INVENTION: Cytoplasmic Bacteriophage Display System

; NUMBER OF SEQUENCES: 70

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brookhaven National Laboratory

; STREET: Building 902C

; CITY: Upton

; STATE: NY

; COUNTRY: US

; ZIP: 11973

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/664,449

; FILING DATE: 17-June-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Bogosian, Margaret
; REGISTRATION NUMBER: 25,324
; REFERENCE/DOCKET NUMBER: AUI-9618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 344-7338
; TELEFAX: (516) 344-3729
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-664-449-37

Query Match 10.3%; Score 4; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AALE 21
|||
Db 25 AALE 28

RESULT 29

US-08-899-575-13

; Sequence 13, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302

; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-899-575-13

Query Match 10.3%; Score 4; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAA 19
|||
Db 14 LLAA 17

RESULT 30
US-08-899-575-13
; Sequence 13, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal

US-08-899-575-13

Query Match 10.3%; Score 4; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAA 19
||||
Db 14 LLAA 17

RESULT 31
US-08-458-568A-6
; Sequence 6, Application US/08458568A
; Patent No. 5821339
; GENERAL INFORMATION:
; APPLICANT: Schaffer, Priscilla A.
; APPLICANT: Yeh, Lily
; TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus
; TITLE OF INVENTION: Infections
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPer2263.1;
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/458,568A
; FILING DATE: 02-JUNE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/065,146
; FILING DATE: 05-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn R.
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: DFCI-0029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-458-568A-6

Query Match 10.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERA 14
|||
Db 10 RERA 13

RESULT 32

US-08-788-231A-18

; Sequence 18, Application US/08788231A
; Patent No. 6019974
; GENERAL INFORMATION:
; APPLICANT: L'Hernault, Steven W.
; TITLE OF INVENTION: SPE-4 RELATED PEPTIDES, ANTIBODIES AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,231A
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/010,672
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 60-95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES

US-08-788-231A-18

Query Match 10.3%; Score 4; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 LLVL 36
|||
Db 19 LLVL 22

RESULT 33

US-09-348-578-3

; Sequence 3, Application US/09348578
; Patent No. 6160089
; GENERAL INFORMATION:
; APPLICANT: HONJO, Masaru
; APPLICANT: NAITOH, Naokazu
; APPLICANT: UCHIDA, Hiroshi
; APPLICANT: MOCHIZUKI, Daisuke
; APPLICANT: MATSUMOTO, Kazuya
; TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF HUMAN GROWTH HORMONE
; FILE REFERENCE: 029430-421
; CURRENT APPLICATION NUMBER: US/09/348,578
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: JP 193003/1998
; EARLIER FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Modified OppA
secretion
; OTHER INFORMATION: signal
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(28)

US-09-348-578-3

Query Match 10.3%; Score 4; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
|||
Db 17 LAAL 20

RESULT 34

US-09-348-578-11

; Sequence 11, Application US/09348578
; Patent No. 6160089
; GENERAL INFORMATION:
; APPLICANT: HONJO, Masaru
; APPLICANT: NAITOH, Naokazu
; APPLICANT: UCHIDA, Hiroshi
; APPLICANT: MOCHIZUKI, Daisuke
; APPLICANT: MATSUMOTO, Kazuya
; TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF HUMAN GROWTH HORMONE
; FILE REFERENCE: 029430-421
; CURRENT APPLICATION NUMBER: US/09/348,578
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: JP 193003/1998
; EARLIER FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(28)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Modified OppA
secretion
; OTHER INFORMATION: signal

US-09-348-578-11

Query Match 10.3%; Score 4; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
|||
Db 17 LAAL 20

RESULT 35

US-09-348-578-19

; Sequence 19, Application US/09348578
; Patent No. 6160089
; GENERAL INFORMATION:
; APPLICANT: HONJO, Masaru

; APPLICANT: NAITOH, Naokazu
; APPLICANT: UCHIDA, Hiroshi
; APPLICANT: MOCHIZUKI, Daisuke
; APPLICANT: MATSUMOTO, Kazuya
; TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF HUMAN GROWTH HORMONE
; FILE REFERENCE: 029430-421
; CURRENT APPLICATION NUMBER: US/09/348,578
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: JP 193003/1998
; EARLIER FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(28)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Modified OppA
secretion
; OTHER INFORMATION: signal
US-09-348-578-19

Query Match 10.3%; Score 4; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
|||
Db 17 LAAL 20

RESULT 36
US-08-974-549A-166
; Sequence 166, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 166:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-974-549A-166

Query Match 10.3%; Score 4; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 LNSY 29
 ||||
Db 7 LNSY 10

RESULT 37
US-09-107-991-12
; Sequence 12, Application US/09107991
; Patent No. 6221626
; GENERAL INFORMATION:
; APPLICANT: Bienvenut, Willy V.
; APPLICANT: Hochstrasser, Denis F.
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts L.L.P.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112-0028
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,991
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seide, Rochelle K. Ph.D.
; REGISTRATION NUMBER: 32,300
; REFERENCE/DOCKET NUMBER: A31855
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)705-5000
; TELEFAX: (212)705-5020
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-107-991-12

Query Match 10.3%; Score 4; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ARLL 17
 ||||
Db 14 ARLL 17

RESULT 38

US-09-041-886-42
; Sequence 42, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-041-886-42

Query Match 10.3%; Score 4; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
|||
Db 22 LAAL 25

RESULT 39
US-09-507-819-30
; Sequence 30, Application US/09507819
; Patent No. 6303314
; GENERAL INFORMATION:
; APPLICANT: Jingwu, Zhang Z.
; TITLE OF INVENTION: T Cell Receptor VB-DBA&B Sequence, a5X0
; Patent No. 6303314

s For Its

; TITLE OF INVENTION: Detection
; FILE REFERENCE: BCOL003
; CURRENT APPLICATION NUMBER: US/09/507,819
; CURRENT FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-507-819-30

Query Match 10.3%; Score 4; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 LLVL 36
||||
Db 20 LLVL 23

RESULT 40

US-09-099-041A-19

; Sequence 19, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-099-041A-19

Query Match 10.3%; Score 4; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
||||
Db 22 LALA 25

Search completed: January 14, 2004, 10:43:44
Job time : 18.243 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 11.5421 Seconds
(without alignments)
324.949 Million cell updates/sec

Title: US-09-843-221A-170

Perfect score: 39

Sequence: 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3709

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : PIR_76:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	5	12.8	29	2	G83440	KdpF protein PA163
2	5	12.8	29	2	A32860	biotin-binding pro
3	5	12.8	31	2	S05124	hypothetical prote
4	5	12.8	31	2	S58569	hypothetical prote
5	5	12.8	31	2	T14568	hypothetical prote
6	5	12.8	33	2	A82451	hypothetical prote
7	5	12.8	38	2	G97576	hypothetical prote
8	4	10.3	28	2	T14210	NADH2 dehydrogenas
9	4	10.3	28	2	S21278	glutathione transf
10	4	10.3	28	2	B35948	phospholipase A2 (
11	4	10.3	28	2	A56366	intestinal trefoil
12	4	10.3	28	2	PH0231	T-cell receptor Vb
13	4	10.3	28	2	T06925	hypothetical prote

14	4	10.3	28	2	JQ1035	hypothetical 3.2K
15	4	10.3	29	2	E47719	house-dust-mite-re
16	4	10.3	29	2	S58390	T-cell receptor be
17	4	10.3	29	2	I37534	gene HLA-DRB prote
18	4	10.3	29	2	I37535	gene HLA-DRB prote
19	4	10.3	29	2	I37536	MHC class II histo
20	4	10.3	29	2	I37301	MHC class II histo
21	4	10.3	29	2	I37303	HLA-DR beta - huma
22	4	10.3	29	2	I37306	HLA-DR beta - huma
23	4	10.3	29	2	S78326	conserved hypothet
24	4	10.3	29	2	S16323	hypothetical prote
25	4	10.3	29	2	S78714	protein YDR524w-a
26	4	10.3	30	2	S21195	spectrin beta chai
27	4	10.3	30	2	S30333	N-carbamoyl-D-amin
28	4	10.3	30	2	E84786	hypothetical prote
29	4	10.3	31	2	PH0236	T-cell receptor Vb
30	4	10.3	31	2	I48082	mitochondrial benz
31	4	10.3	31	2	S76281	hypothetical prote
32	4	10.3	31	2	S74965	photosystem I reac
33	4	10.3	31	2	D82827	hypothetical prote
34	4	10.3	31	2	T07290	photosystem I prot
35	4	10.3	32	2	D61014	defensin NP-1 - ra
36	4	10.3	32	2	E61014	defensin R-5 - rat
37	4	10.3	32	2	A25735	interphotoreceptor
38	4	10.3	32	2	C84355	hypothetical prote
39	4	10.3	32	2	PC7067	meltrin beta - mou
40	4	10.3	33	2	A44181	Cerastes serine pr
41	4	10.3	33	2	B56635	tubulin alpha chai
42	4	10.3	33	2	A05010	hypothetical prote
43	4	10.3	33	2	H95094	hypothetical prote
44	4	10.3	33	2	PC7035	reversion inducing
45	4	10.3	33	2	E45557	orf immediately up
46	4	10.3	33	2	A82288	hypothetical prote
47	4	10.3	33	2	F97371	hypothetical prote
48	4	10.3	34	2	S71457	NADH2 dehydrogenas
49	4	10.3	34	2	C56635	tubulin alpha chai
50	4	10.3	34	2	A84391	hypothetical prote
51	4	10.3	35	2	A05112	M24 protein - Stre
52	4	10.3	35	2	S65772	early nodulin 40 -
53	4	10.3	35	2	A81346	hypothetical prote
54	4	10.3	35	2	D97553	hypothetical prote
55	4	10.3	35	2	AI1823	photosystem II Psb
56	4	10.3	36	2	S70806	hypothetical prote
57	4	10.3	36	2	D87544	hypothetical prote
58	4	10.3	36	2	E70238	hypothetical prote
59	4	10.3	36	2	A41017	LDL receptor-relat
60	4	10.3	36	2	A61316	largomycin - Strep
61	4	10.3	37	2	C45187	homeotic protein G
62	4	10.3	37	2	C84210	hypothetical prote
63	4	10.3	37	2	H72308	hypothetical prote
64	4	10.3	37	2	F82102	hypothetical prote
65	4	10.3	37	2	A57127	diuretic hormone 1
66	4	10.3	37	2	H83756	hypothetical prote
67	4	10.3	37	2	JC6153	viral capsid prote
68	4	10.3	38	2	T11763	acetyl-CoA carboxy
69	4	10.3	38	2	B82413	hypothetical prote
70	4	10.3	38	2	T34678	hypothetical prote

71	4	10.3	38	2	E37334	alcohol dehydrogen
72	4	10.3	39	2	S51003	hypothetical prote
73	4	10.3	39	2	B87458	hypothetical prote
74	4	10.3	39	2	B82452	hypothetical prote
75	4	10.3	39	2	E69677	phosphatase (RapI)
76	4	10.3	39	2	F82767	hypothetical prote
77	4	10.3	39	2	C85911	hypothetical prote
78	4	10.3	40	2	S39822	hypothetical prote
79	4	10.3	40	2	S43028	ribosomal protein
80	4	10.3	40	2	A64530	hypothetical prote
81	4	10.3	40	2	D83378	hypothetical prote
82	4	10.3	40	2	S01102	hypothetical prote
83	3	7.7	28	2	S71598	cytochrome P450 HP
84	3	7.7	28	2	S04341	cytochrome P450 PB
85	3	7.7	28	2	PX0033	cytochrome P450 te
86	3	7.7	28	2	S66436	allophycocyanin al
87	3	7.7	28	2	T12301	NADH2 dehydrogenas
88	3	7.7	28	2	A34244	hexokinase (EC 2.7
89	3	7.7	28	2	A31859	deoxycytidine kina
90	3	7.7	28	2	A38296	sterol esterase (E
91	3	7.7	28	2	A35115	hypothetical prote
92	3	7.7	28	2	S55729	orotidine-5'-monop
93	3	7.7	28	2	A61322	somatostatin-28 -
94	3	7.7	28	2	B60071	vasoactive intesti
95	3	7.7	28	2	A60304	vasoactive intesti
96	3	7.7	28	2	A38232	vasoactive intesti
97	3	7.7	28	2	A60303	vasoactive intesti
98	3	7.7	28	2	JT0412	bombyxin-IV chain
99	3	7.7	28	2	A49829	T-cell receptor va
100	3	7.7	28	2	S11618	ribosomal protein
101	3	7.7	28	2	I50169	alpha-1 type-1 col
102	3	7.7	28	2	S55442	beta A2 crystallin
103	3	7.7	28	2	I48349	fibronectin - mous
104	3	7.7	28	2	F54346	pyruvate synthase
105	3	7.7	28	2	S29135	aminopyrine N-deme
106	3	7.7	28	2	S29136	aminopyrine N-deme
107	3	7.7	28	2	PN0625	homeobox JRX prote
108	3	7.7	28	2	B56779	tetM 5'-region lea
109	3	7.7	28	2	B47310	MHVS28AA - murine
110	3	7.7	28	2	S15235	hypothetical prote
111	3	7.7	28	2	I60364	phosphorybosylpyro
112	3	7.7	28	2	S70894	hypothetical prote
113	3	7.7	28	2	B39191	hypothetical prote
114	3	7.7	28	2	S63502	95K protein - Euba
115	3	7.7	28	2	T14905	hypothetical prote
116	3	7.7	28	2	JQ0272	hypothetical 3K pr
117	3	7.7	28	2	A44923	carboxypeptidase 3
118	3	7.7	28	2	A60698	trichocyst protein
119	3	7.7	28	2	A27261	proteinase inhibit
120	3	7.7	28	2	I59477	antigen, T-cell re
121	3	7.7	28	2	S54338	cytochrome P450 CY
122	3	7.7	28	2	I52627	erythrocyte chemok
123	3	7.7	28	2	PH1335	Ig heavy chain DJ
124	3	7.7	28	2	PT0366	T-cell receptor be
125	3	7.7	28	2	I58115	cystic fibrosis tr
126	3	7.7	28	2	B83797	hypothetical prote
127	3	7.7	28	2	C83797	hypothetical prote

128	3	7.7	28	2	C83969	hypothetical prote
129	3	7.7	28	2	S51593	myrB protein - Mic
130	3	7.7	28	2	H85908	hypothetical prote
131	3	7.7	28	4	JN0014	GABA(A) receptor a
132	3	7.7	29	1	Q1BP57	gene 1.5 protein -
133	3	7.7	29	2	A60558	cytochrome P450 HL
134	3	7.7	29	2	A48427	flavohemoglobin hm
135	3	7.7	29	2	PC2364	protoporphyrinogen
136	3	7.7	29	2	S08201	peroxidase (EC 1.1
137	3	7.7	29	2	S39968	probable hydro-lya
138	3	7.7	29	2	S28174	heat-shock protein
139	3	7.7	29	2	S17432	H+-transporting tw
140	3	7.7	29	2	T03653	phospholipid trans
141	3	7.7	29	2	A39462	cholestokinin - do
142	3	7.7	29	2	S17147	galanin - chicken
143	3	7.7	29	2	I52628	low affinity nerve
144	3	7.7	29	2	C61233	conceptus protein
145	3	7.7	29	2	C47719	T-cell receptor al
146	3	7.7	29	2	S10050	ribosomal protein
147	3	7.7	29	2	S26229	ribosomal protein
148	3	7.7	29	2	S10725	calmodulin-binding
149	3	7.7	29	2	S57232	homeotic protein s
150	3	7.7	29	2	T51116	probable precorrin
151	3	7.7	29	2	B34490	lens fiber cell me
152	3	7.7	29	2	A35121	hypothetical prote
153	3	7.7	29	2	G90719	hypothetical prote
154	3	7.7	29	2	S14040	hypothetical prote
155	3	7.7	29	2	G64674	hypothetical prote
156	3	7.7	29	2	T48910	KdpF protein [vali
157	3	7.7	29	2	S65747	CDP-paratose synth
158	3	7.7	29	2	S65748	CDP-paratose synth
159	3	7.7	29	2	S05224	photosystem I 4.8K
160	3	7.7	29	2	S74572	hypothetical prote
161	3	7.7	29	2	S67989	HA-19/HA-52 protei
162	3	7.7	29	2	S77569	plantaricin SA6 -
163	3	7.7	29	2	B41476	probable antigen 2
164	3	7.7	29	2	S03947	hydrogen dehydroge
165	3	7.7	29	2	T37120	hypothetical prote
166	3	7.7	29	2	T36654	probable small mem
167	3	7.7	29	2	B43937	endo-1,4-beta-xyla
168	3	7.7	29	2	T06904	hypothetical prote
169	3	7.7	29	2	S73197	hypothetical prote
170	3	7.7	29	2	S78360	hypothetical prote
171	3	7.7	29	2	S01572	hypothetical prote
172	3	7.7	29	2	T07450	hypothetical prote
173	3	7.7	29	2	S01448	hypothetical prote
174	3	7.7	29	2	S43992	peroxidase (EC 1.1
175	3	7.7	29	2	JQ0212	hypothetical 3K pr
176	3	7.7	29	2	S58541	hypothetical prote
177	3	7.7	29	2	S68094	2,3-dihydroxybenzo
178	3	7.7	29	2	B21112	variant surface gl
179	3	7.7	29	2	B60698	trichocyst protein
180	3	7.7	29	2	A61613	ceratotoxin A - Me
181	3	7.7	29	2	B61613	ceratotoxin B - Me
182	3	7.7	29	2	I50695	non-collagenous al
183	3	7.7	29	2	I77372	CD44SP - human
184	3	7.7	29	2	C54037	splicing regulator

185	3	7.7	29	2	S57204	oviduct-specific s
186	3	7.7	29	2	S38749	vimentin homolog -
187	3	7.7	29	2	A83923	hypothetical prote
188	3	7.7	29	2	B85840	hypothetical prote
189	3	7.7	29	2	C85840	hypothetical prote
190	3	7.7	29	2	AH2338	PetN protein [impo
191	3	7.7	30	1	TIPU1W	trypsin inhibitor
192	3	7.7	30	1	CLHRY2	protamine YII - Pa
193	3	7.7	30	1	CLHR2A	protamine YII - At
194	3	7.7	30	2	I57689	ubiquinol-cytochro
195	3	7.7	30	2	PQ0723	parvalbumin [impor
196	3	7.7	30	2	S08202	peroxidase (EC 1.1
197	3	7.7	30	2	S08204	peroxidase (EC 1.1
198	3	7.7	30	2	S08203	peroxidase (EC 1.1
199	3	7.7	30	2	C21897	ornithine carbamoy
200	3	7.7	30	2	A28562	glutathione transf
201	3	7.7	30	2	A27103	aspartate transami
202	3	7.7	30	2	I55427	aspartate transami
203	3	7.7	30	2	S68639	nigroxin A - black
204	3	7.7	30	2	S68640	nigroxin B - black
205	3	7.7	30	2	PX0073	epoxide hydrolase
206	3	7.7	30	2	A61333	trypsin (EC 3.4.21
207	3	7.7	30	2	S60893	InvC protein - Sal
208	3	7.7	30	2	S24979	proteinase inhibit
209	3	7.7	30	2	JX0057	trypsin inhibitor
210	3	7.7	30	2	A61130	somatotropin - Ame
211	3	7.7	30	2	A59076	defensin alpha-1 -
212	3	7.7	30	2	B59076	defensin alpha-2 -
213	3	7.7	30	2	C59076	defensin alpha-3 -
214	3	7.7	30	2	I68109	interferon alpha-W
215	3	7.7	30	2	PH0237	T-cell receptor Vb
216	3	7.7	30	2	PH0882	Ig kappa chain V r
217	3	7.7	30	2	A21680	hemoglobin epsilon
218	3	7.7	30	2	A05254	hemoglobin epsilon
219	3	7.7	30	2	S07217	ribosomal protein
220	3	7.7	30	2	I52806	Duchenne muscular
221	3	7.7	30	2	B61511	serum albumin, mil
222	3	7.7	30	2	S57234	fushi tarazu segme
223	3	7.7	30	2	S07065	rRNA N-glycosidase
224	3	7.7	30	2	A31836	17K antigen - Rick
225	3	7.7	30	2	A22977	delta-endotoxin -
226	3	7.7	30	2	A44913	34K core flagella
227	3	7.7	30	2	S08565	ribulose-bisphosph
228	3	7.7	30	2	S30757	genome polyprotein
229	3	7.7	30	2	S30759	genome polyprotein
230	3	7.7	30	2	B44314	intracisternal A p
231	3	7.7	30	2	I58367	gag protein - mous
232	3	7.7	30	2	S42364	aromatic-amino-aci
233	3	7.7	30	2	PS0437	potassium channel
234	3	7.7	30	2	PQ0444	hypothetical prote
235	3	7.7	30	2	C95030	hypothetical prote
236	3	7.7	30	2	F95118	hypothetical prote
237	3	7.7	30	2	A84412	hypothetical prote
238	3	7.7	30	2	S15141	hypothetical prote
239	3	7.7	30	2	D72276	hypothetical prote
240	3	7.7	30	2	E72356	hypothetical prote
241	3	7.7	30	2	H72312	hypothetical prote

242	3	7.7	30	2	D70253	conserved hypothet
243	3	7.7	30	2	H70152	hypothetical prote
244	3	7.7	30	2	B70165	hypothetical prote
245	3	7.7	30	2	A70209	hypothetical prote
246	3	7.7	30	2	H64522	hypothetical prote
247	3	7.7	30	2	S14365	4-sulfobenzoate 3,
248	3	7.7	30	2	A83556	hypothetical prote
249	3	7.7	30	2	S30347	4-hydroxybenzoyl-C
250	3	7.7	30	2	B81889	hypothetical prote
251	3	7.7	30	2	A36733	hypothetical prote
252	3	7.7	30	2	C82341	hypothetical prote
253	3	7.7	30	2	A82137	hypothetical prote
254	3	7.7	30	2	C82092	hypothetical prote
255	3	7.7	30	2	H82510	hypothetical prote
256	3	7.7	30	2	B82428	hypothetical prote
257	3	7.7	30	2	S78303	photosystem I prot
258	3	7.7	30	2	S19609	glucooligosacchari
259	3	7.7	30	2	D32946	serine proteinase
260	3	7.7	30	2	B60914	pheromone-binding
261	3	7.7	30	2	A61546	beta-N-acetylgluco
262	3	7.7	30	2	S23365	T-cell receptor al
263	3	7.7	30	2	B46958	androgen-binding p
264	3	7.7	30	2	S48114	cystic fibrosis tr
265	3	7.7	30	2	B84053	hypothetical prote
266	3	7.7	30	2	C71309	hypothetical prote
267	3	7.7	30	2	G82515	hypothetical prote
268	3	7.7	30	2	A48923	retrovirus-related
269	3	7.7	30	2	E85694	hypothetical prote
270	3	7.7	30	2	F89864	hypothetical prote
271	3	7.7	30	2	S34761	L-serine ammonia-l
272	3	7.7	31	1	CLHRZ	protamine Z - Paci
273	3	7.7	31	1	CLHRZA	protamine Z - Atla
274	3	7.7	31	1	JU0351	3.6K protein - Chl
275	3	7.7	31	1	D64117	ftsH protein homol
276	3	7.7	31	1	S34504	photosystem I prot
277	3	7.7	31	2	S13205	glyceraldehyde-3-p
278	3	7.7	31	2	S18356	chymotrypsin (EC 3
279	3	7.7	31	2	S61558	chymotrypsin Pm1 -
280	3	7.7	31	2	PC1269	subtilisin inhibit
281	3	7.7	31	2	S21743	trypsin inhibitor
282	3	7.7	31	2	S39019	glucagon-like pept
283	3	7.7	31	2	F30608	Ig kappa chain V-I
284	3	7.7	31	2	D30608	Ig kappa chain V-I
285	3	7.7	31	2	E53480	T-cell receptor al
286	3	7.7	31	2	S03297	Ig alpha chain C r
287	3	7.7	31	2	A34448	myosin heavy chain
288	3	7.7	31	2	A20883	variant surface gl
289	3	7.7	31	2	I39679	exeE protein - Aer
290	3	7.7	31	2	S03336	photosystem II pro
291	3	7.7	31	2	B41453	translation elonga
292	3	7.7	31	2	S53132	gene X protein - h
293	3	7.7	31	2	S53135	gene X protein - h
294	3	7.7	31	2	S53138	gene X protein - h
295	3	7.7	31	2	S53141	gene X protein - h
296	3	7.7	31	2	S53147	gene X protein - h
297	3	7.7	31	2	S53150	gene X protein - h
298	3	7.7	31	2	S53153	gene X protein - h

299	3	7.7	31	2	S53156	gene X protein - h
300	3	7.7	31	2	S53160	gene X protein - h
301	3	7.7	31	2	S53162	gene X protein - h
302	3	7.7	31	2	S53164	gene X protein - h
303	3	7.7	31	2	S53176	gene X protein - h
304	3	7.7	31	2	S53179	gene X protein - h
305	3	7.7	31	2	S53187	gene X protein - h
306	3	7.7	31	2	S53190	gene X protein - h
307	3	7.7	31	2	S53192	gene X protein - h
308	3	7.7	31	2	S53199	gene X protein - h
309	3	7.7	31	2	S53201	gene X protein - h
310	3	7.7	31	2	S53205	gene X protein - h
311	3	7.7	31	2	S53208	gene X protein - h
312	3	7.7	31	2	S53215	gene X protein - h
313	3	7.7	31	2	S53219	gene X protein - h
314	3	7.7	31	2	S53228	gene X protein - h
315	3	7.7	31	2	S53254	gene X protein - h
316	3	7.7	31	2	S53258	gene X protein - h
317	3	7.7	31	2	S53282	gene X protein - h
318	3	7.7	31	2	S53284	gene X protein - h
319	3	7.7	31	2	S53287	gene X protein - h
320	3	7.7	31	2	S53289	gene X protein - h
321	3	7.7	31	2	D34490	lens fiber cell me
322	3	7.7	31	2	T36124	hypothetical prote
323	3	7.7	31	2	S65418	pyruvate synthase
324	3	7.7	31	2	C54346	pyruvate synthase
325	3	7.7	31	2	A23341	allergen R7 - pere
326	3	7.7	31	2	C95010	hypothetical prote
327	3	7.7	31	2	G95022	hypothetical prote
328	3	7.7	31	2	A95237	hypothetical prote
329	3	7.7	31	2	H72808	gp82.2 protein - M
330	3	7.7	31	2	S40665	hypothetical prote
331	3	7.7	31	2	C48472	capsid protein VP-
332	3	7.7	31	2	F72270	hypothetical prote
333	3	7.7	31	2	E70223	hypothetical prote
334	3	7.7	31	2	C71845	hypothetical prote
335	3	7.7	31	2	B81027	lacto-N-neotetraos
336	3	7.7	31	2	T08489	hypothetical prote
337	3	7.7	31	2	C82175	hypothetical prote
338	3	7.7	31	2	B82138	hypothetical prote
339	3	7.7	31	2	G82071	hypothetical prote
340	3	7.7	31	2	G82066	hypothetical prote
341	3	7.7	31	2	E82466	hypothetical prote
342	3	7.7	31	2	S31075	hypothetical prote
343	3	7.7	31	2	S16049	photosystem I prot
344	3	7.7	31	2	T46840	hypothetical prote
345	3	7.7	31	2	T36103	hypothetical prote
346	3	7.7	31	2	T36022	small hypothetical
347	3	7.7	31	2	T06934	photosystem I chai
348	3	7.7	31	2	T06854	photosystem II pro
349	3	7.7	31	2	S73244	photosystem II pro
350	3	7.7	31	2	S78335	hypothetical prote
351	3	7.7	31	2	A53841	ycf8 protein - Eug
352	3	7.7	31	2	S20491	hypothetical prote
353	3	7.7	31	2	A05051	hypothetical prote
354	3	7.7	31	2	B20883	variant surface gl
355	3	7.7	31	2	T16215	hypothetical prote

356	3	7.7	31	2	G24802	cuticle protein 54
357	3	7.7	31	2	B60363	apolipoporphin III
358	3	7.7	31	2	B42176	insulin-like growth
359	3	7.7	31	2	I61697	myosin - human (fr)
360	3	7.7	31	2	I46598	myosin - pig (frag)
361	3	7.7	31	2	I46276	hemoglobin beta-x
362	3	7.7	31	2	S27112	sarcolipin - rabbi
363	3	7.7	31	2	T09121	hypothetical protein
364	3	7.7	31	2	G82766	hypothetical protein
365	3	7.7	31	2	C82620	hypothetical protein
366	3	7.7	31	2	T07276	photosystem II protein
367	3	7.7	31	2	B85582	unknown protein encoded
368	3	7.7	31	2	AB0049	transposase (parti
369	3	7.7	31	2	AD2046	hypothetical protein
370	3	7.7	32	1	TCEE	calcitonin - Japan
371	3	7.7	32	1	TCON2	calcitonin 2 - soc
372	3	7.7	32	1	TCON2C	calcitonin 2 - chu
373	3	7.7	32	1	TCON2P	calcitonin 2 - pin
374	3	7.7	32	1	TCON3	calcitonin 3 - coh
375	3	7.7	32	1	IRTR2	protamine II - rai
376	3	7.7	32	1	LFECI	ilvGMEDA operon leader
377	3	7.7	32	1	LFEBIT	peptide
378	3	7.7	32	1	LFECIV	ilvBN operon leader
379	3	7.7	32	2	JT0017	ferredoxin [2Fe-2S]
380	3	7.7	32	2	S20719	alcohol dehydrogen
381	3	7.7	32	2	A56672	methylguanidine-sy
382	3	7.7	32	2	S35583	glutathione transf
383	3	7.7	32	2	G46376	1-aminocyclopropan
384	3	7.7	32	2	A32502	T-cell receptor de
385	3	7.7	32	2	E60505	hemoglobin A2-3 beta
386	3	7.7	32	2	S05455	histone H2A - brin
387	3	7.7	32	2	I51089	protamine - Japane
388	3	7.7	32	2	A02687	DNA-binding protei
389	3	7.7	32	2	S51061	ribosomal protein
390	3	7.7	32	2	A24047	gap junction prote
391	3	7.7	32	2	S72220	alpha-S1-casein -
392	3	7.7	32	2	S36809	GTP-binding regula
393	3	7.7	32	2	A61052	heat shock protein
394	3	7.7	32	2	I48415	heat shock factor
395	3	7.7	32	2	A59156	gliadin omega-5 -
396	3	7.7	32	2	E91216	ilvGEDA operon lea
397	3	7.7	32	2	F86062	ilvGMEDA operon le
398	3	7.7	32	2	AG0924	ilvGMEDA operon at
399	3	7.7	32	2	E91205	ilvB operon leader
400	3	7.7	32	2	G86051	ilvBN operon leader
401	3	7.7	32	2	A44906	L1 protein - human
402	3	7.7	32	2	S19906	E6-II protein - hu
403	3	7.7	32	2	PQ0425	nonstructural protein
404	3	7.7	32	2	PQ0413	nonstructural protein
405	3	7.7	32	2	PQ0419	nonstructural protein
406	3	7.7	32	2	C58493	group I allergen A
407	3	7.7	32	2	B58493	group I allergen A
408	3	7.7	32	2	S03273	photosystem II oxy
409	3	7.7	32	2	C46107	polyomavirus enhan
410	3	7.7	32	2	S57228	zen protein (clone
411	3	7.7	32	2	A95108	hypothetical protein
412	3	7.7	32	2	A95137	hypothetical protein

413	3	7.7	32	2	G95225	hypothetical prote
414	3	7.7	32	2	E87701	hypothetical prote
415	3	7.7	32	2	G84161	hypothetical prote
416	3	7.7	32	2	H70153	hypothetical prote
417	3	7.7	32	2	D70222	hypothetical prote
418	3	7.7	32	2	E70225	hypothetical prote
419	3	7.7	32	2	G70249	hypothetical prote
420	3	7.7	32	2	B70257	hypothetical prote
421	3	7.7	32	2	D55230	phosphoenolpyruvat
422	3	7.7	32	2	E82279	hypothetical prote
423	3	7.7	32	2	F82097	hypothetical prote
424	3	7.7	32	2	C82467	hypothetical prote
425	3	7.7	32	2	B82421	hypothetical prote
426	3	7.7	32	2	H82416	hypothetical prote
427	3	7.7	32	2	F82407	hypothetical prote
428	3	7.7	32	2	S23476	hypothetical prote
429	3	7.7	32	2	S07713	hypothetical prote
430	3	7.7	32	2	S22304	hypothetical prote
431	3	7.7	32	2	T36275	hypothetical prote
432	3	7.7	32	2	S73196	hypothetical prote
433	3	7.7	32	2	S78323	photosystem II pro
434	3	7.7	32	2	A05015	hypothetical prote
435	3	7.7	32	2	B38578	protein kinase 1 (
436	3	7.7	32	2	S35053	L-mandelate dehydr
437	3	7.7	32	2	S36825	UDP-galactose-N-ac
438	3	7.7	32	2	A61624	apolipophorin-III
439	3	7.7	32	2	F82833	hypothetical prote
440	3	7.7	32	2	E85588	hypothetical prote
441	3	7.7	32	2	S78776	imelysin (EC 3.4.2
442	3	7.7	32	2	AB0774	hypothetical prote
443	3	7.7	33	1	A23483	alcohol oxidase (E
444	3	7.7	33	1	WRECP1	protamine-like pro
445	3	7.7	33	1	FDFI5G	antifreeze protein
446	3	7.7	33	2	A36154	benzphetamine N-de
447	3	7.7	33	2	JT0022	ferredoxin [2Fe-2S
448	3	7.7	33	2	B60743	ornithine carbamoy
449	3	7.7	33	2	S41916	DNA-directed RNA p
450	3	7.7	33	2	S43312	2',3'-cyclic-nucle
451	3	7.7	33	2	A56818	Na+/K+-exchanging
452	3	7.7	33	2	PC2249	peptidylprolyl iso
453	3	7.7	33	2	PC1270	subtilisin inhibit
454	3	7.7	33	2	PC2205	interferon-alpha L
455	3	7.7	33	2	E32502	T-cell receptor de
456	3	7.7	33	2	A31461	T-cell receptor de
457	3	7.7	33	2	A61310	nonhistone chromos
458	3	7.7	33	2	C21211	protamine TP16 - r
459	3	7.7	33	2	E21211	protamine TP21 - r
460	3	7.7	33	2	A26762	protamine (mugilin
461	3	7.7	33	2	B26762	protamine (mugilin
462	3	7.7	33	2	A60601	keratin, 55k, nucl
463	3	7.7	33	2	S50032	lysosomal-associat
464	3	7.7	33	2	A05162	antifreeze protein
465	3	7.7	33	2	I52083	major acute phase
466	3	7.7	33	2	T43305	translation initia
467	3	7.7	33	2	B44906	L1 protein - human
468	3	7.7	33	2	S23321	hypothetical prote
469	3	7.7	33	2	T36211	probable excisiona

470	3	7.7	33	2	I22565	R-phycoerythrin ga
471	3	7.7	33	2	D44798	alkylphosphonate u
472	3	7.7	33	2	S06337	teleocalcin - rain
473	3	7.7	33	2	T08018	ycf12 protein - Ch
474	3	7.7	33	2	I68894	gene TAP1 protein
475	3	7.7	33	2	A87213	hypothetical prote
476	3	7.7	33	2	E84341	hypothetical prote
477	3	7.7	33	2	E43675	orf protein - infe
478	3	7.7	33	2	A70159	hypothetical prote
479	3	7.7	33	2	G70247	hypothetical prote
480	3	7.7	33	2	S61846	hrpY protein - Pse
481	3	7.7	33	2	C82312	hypothetical prote
482	3	7.7	33	2	D82309	hypothetical prote
483	3	7.7	33	2	C82287	hypothetical prote
484	3	7.7	33	2	G82254	hypothetical prote
485	3	7.7	33	2	H82216	hypothetical prote
486	3	7.7	33	2	B82184	hypothetical prote
487	3	7.7	33	2	H82475	hypothetical prote
488	3	7.7	33	2	E82391	hypothetical prote
489	3	7.7	33	2	C82390	hypothetical prote
490	3	7.7	33	2	S63523	formylmethanofuran
491	3	7.7	33	2	T46624	hypothetical prote
492	3	7.7	33	2	A41822	antimicrobial pept
493	3	7.7	33	2	S58578	hypothetical prote
494	3	7.7	33	2	T39160	hypothetical prote
495	3	7.7	33	2	I51869	neurofibromin - hu
496	3	7.7	33	2	S32764	T-cell receptor ga
497	3	7.7	33	2	H43284	zinc finger protei
498	3	7.7	33	2	S68096	lactate dehydrogen
499	3	7.7	33	2	I53301	gene GHR protein -
500	3	7.7	33	2	T03346	gene e21 protein -
501	3	7.7	33	2	E82852	hypothetical prote
502	3	7.7	33	2	E82553	hypothetical prote
503	3	7.7	33	2	C86007	hypothetical prote
504	3	7.7	33	2	F85581	unknown protein en
505	3	7.7	33	2	G86126	hypothetical prote
506	3	7.7	33	2	D89945	hypothetical prote
507	3	7.7	33	2	B81295	probable periplasm
508	3	7.7	33	2	I37258	NADH2 dehydrogenas
509	3	7.7	33	2	C97406	hypothetical prote
510	3	7.7	34	1	LNBOC1	pulmonary surfacta
511	3	7.7	34	2	S27176	cytochrome P450 2E
512	3	7.7	34	2	A12055	glyceraldehyde-3-p
513	3	7.7	34	2	A60475	glyceraldehyde-3-p
514	3	7.7	34	2	S18161	NADH2 dehydrogenas
515	3	7.7	34	2	A60686	cytochrome-c oxida
516	3	7.7	34	2	S62710	cytochrome-c oxida
517	3	7.7	34	2	A28506	pyruvate kinase (E
518	3	7.7	34	2	S08196	3-dehydroquinate d
519	3	7.7	34	2	I40771	enolase - Campylob
520	3	7.7	34	2	PC1272	subtilisin inhibit
521	3	7.7	34	2	PC1261	alkaline proteinas
522	3	7.7	34	2	PC1267	subtilisin inhibit
523	3	7.7	34	2	A61491	seed protein ws-1
524	3	7.7	34	2	A32271	somatostatin-relat
525	3	7.7	34	2	A40298	dermaseptin - Sauv
526	3	7.7	34	2	C49195	corticostatic pept

527	3	7.7	34	2	A19197	class II histocomp
528	3	7.7	34	2	D60505	hemoglobin A1-4 be
529	3	7.7	34	2	JN0582	protamine (scombro
530	3	7.7	34	2	S20439	protamine - yellow
531	3	7.7	34	2	S56118	myosin II heavy ch
532	3	7.7	34	2	A05330	colipase - chicken
533	3	7.7	34	2	S65716	prostaglandin-D sy
534	3	7.7	34	2	E49410	t-complex polypept
535	3	7.7	34	2	S13439	lectin II, anti-H(
536	3	7.7	34	2	A44806	variant surface gl
537	3	7.7	34	2	S11866	transposase - pear
538	3	7.7	34	2	PS0065	lysis protein t -
539	3	7.7	34	2	D58493	group I allergen D
540	3	7.7	34	2	B60106	type-specific anti
541	3	7.7	34	2	S78345	hypothetical prote
542	3	7.7	34	2	I50713	homeobox protein -
543	3	7.7	34	2	I51364	homeobox protein -
544	3	7.7	34	2	I38900	homeobox protein -
545	3	7.7	34	2	I49145	homeobox protein -
546	3	7.7	34	2	I65263	homeobox protein H
547	3	7.7	34	2	F95129	hypothetical prote
548	3	7.7	34	2	D95208	hypothetical prote
549	3	7.7	34	2	G90912	hypothetical prote
550	3	7.7	34	2	C90973	hypothetical prote
551	3	7.7	34	2	F84466	hypothetical prote
552	3	7.7	34	2	B70230	hypothetical prote
553	3	7.7	34	2	D70249	hypothetical prote
554	3	7.7	34	2	E70255	hypothetical prote
555	3	7.7	34	2	H64666	hypothetical prote
556	3	7.7	34	2	H81883	hypothetical prote
557	3	7.7	34	2	T08490	hypothetical prote
558	3	7.7	34	2	E82284	hypothetical prote
559	3	7.7	34	2	A82048	hypothetical prote
560	3	7.7	34	2	E82458	hypothetical prote
561	3	7.7	34	2	B82449	hypothetical prote
562	3	7.7	34	2	G82415	hypothetical prote
563	3	7.7	34	2	B64015	hypothetical prote
564	3	7.7	34	2	S77646	hypothetical prote
565	3	7.7	34	2	T11814	hypothetical prote
566	3	7.7	34	2	S70330	endosperm protein,
567	3	7.7	34	2	T14642	AW19 protein - sor
568	3	7.7	34	2	S58636	hypothetical prote
569	3	7.7	34	2	A48972	mannose-specific l
570	3	7.7	34	2	S35375	brlA protein - Eme
571	3	7.7	34	2	T19865	hypothetical prote
572	3	7.7	34	2	C31514	hemopexin - chicke
573	3	7.7	34	2	S35923	T-cell receptor ga
574	3	7.7	34	2	F84079	hypothetical prote
575	3	7.7	34	2	B81537	hypothetical prote
576	3	7.7	34	2	E82819	hypothetical prote
577	3	7.7	34	2	B85678	unknown protein en
578	3	7.7	34	2	G85820	unknown protein en
579	3	7.7	34	2	AB2400	cytochrome b6-f co
580	3	7.7	34	4	JT0745	hypothetical trans
581	3	7.7	35	1	HWGHD	exendin-2 - Gila m
582	3	7.7	35	1	LNPGC1	pulmonary surfacta
583	3	7.7	35	1	LNDGC1	pulmonary surfacta

584	3	7.7	35	2	A56859	fatty acid omega-h
585	3	7.7	35	2	S00115	cytochrome-c oxidase
586	3	7.7	35	2	S29729	manganese(II) peroxidase
587	3	7.7	35	2	A54257	deoxynucleoside kinase
588	3	7.7	35	2	S51708	thioglucosidase (E)
589	3	7.7	35	2	JN0369	microbial serine protease
590	3	7.7	35	2	S42876	probable succinate
591	3	7.7	35	2	D23454	ovalbumin phosphoprotein
592	3	7.7	35	2	S54329	elastase inhibitor
593	3	7.7	35	2	B44800	cryptdin 12 - mouse
594	3	7.7	35	2	I48893	cryptdin-10 - mouse
595	3	7.7	35	2	I48894	cryptdin-11 - mouse
596	3	7.7	35	2	I48898	cryptdin-16 - mouse
597	3	7.7	35	2	E38601	Ig kappa chain V region
598	3	7.7	35	2	A05302	hemoglobin beta chain
599	3	7.7	35	2	S27154	ribosomal protein
600	3	7.7	35	2	S07437	ribosomal protein
601	3	7.7	35	2	I55263	alpha-smooth muscle
602	3	7.7	35	2	I39969	outer membrane protein
603	3	7.7	35	2	S61547	transferrin bindin
604	3	7.7	35	2	S19909	E6-III protein - human
605	3	7.7	35	2	PQ0128	hydrogenase maturation
606	3	7.7	35	2	T07870	major latex protein
607	3	7.7	35	2	B33770	hypothetical protein
608	3	7.7	35	2	A58493	group I allergen F
609	3	7.7	35	2	F58493	group I allergen A
610	3	7.7	35	2	E58493	group I allergen P
611	3	7.7	35	2	G58493	group I allergen A
612	3	7.7	35	2	PS0439	potassium channel
613	3	7.7	35	2	S20042	hypothetical protein
614	3	7.7	35	2	E64108	protein V6, truncated
615	3	7.7	35	2	H95010	hypothetical protein
616	3	7.7	35	2	F95028	hypothetical protein
617	3	7.7	35	2	F95049	hypothetical protein
618	3	7.7	35	2	H95156	hypothetical protein
619	3	7.7	35	2	B95157	hypothetical protein
620	3	7.7	35	2	F87622	hypothetical protein
621	3	7.7	35	2	B84674	hypothetical protein
622	3	7.7	35	2	H84214	hypothetical protein
623	3	7.7	35	2	C84398	hypothetical protein
624	3	7.7	35	2	S33666	hypothetical protein
625	3	7.7	35	2	B41161	29K antigen PEB2 -
626	3	7.7	35	2	S27307	surface-array protein
627	3	7.7	35	2	C82149	conserved hypothetical
628	3	7.7	35	2	D82137	hypothetical protein
629	3	7.7	35	2	F82051	hypothetical protein
630	3	7.7	35	2	B82494	hypothetical protein
631	3	7.7	35	2	B82432	hypothetical protein
632	3	7.7	35	2	S38791	hypothetical protein
633	3	7.7	35	2	JQ2236	hypothetical 4.1K
634	3	7.7	35	2	A05057	hypothetical protein
635	3	7.7	35	2	T07509	photosystem II protein
636	3	7.7	35	2	T10249	lectin homolog 1 -
637	3	7.7	35	2	A33708	thionin, cell wall
638	3	7.7	35	2	JQ0254	hypothetical 4K protein
639	3	7.7	35	2	T06314	alpha-amylase homolog
640	3	7.7	35	2	T15713	hypothetical protein

641	3	7.7	35	2	I47076	elastin - sheep (f
642	3	7.7	35	2	A61375	basic fibroblast g
643	3	7.7	35	2	E83824	hypothetical prote
644	3	7.7	35	2	D83924	hypothetical prote
645	3	7.7	35	2	H84034	hypothetical prote
646	3	7.7	35	2	B81570	hypothetical prote
647	3	7.7	35	2	S11614	ribosomal protein
648	3	7.7	35	2	B85708	unknown protein en
649	3	7.7	35	2	F85847	unknown protein en
650	3	7.7	35	2	AI0076	hypothetical prote
651	3	7.7	35	2	A97417	hypothetical prote
652	3	7.7	35	2	AE3041	conserved hypothet
653	3	7.7	35	2	AD2525	hypothetical prote
654	3	7.7	35	4	S41911	hypothetical prote
655	3	7.7	36	1	PCPG	pancreatic hormone
656	3	7.7	36	1	NYPGY	neuropeptide Y - p
657	3	7.7	36	1	PCGXAA	pancreatic peptide
658	3	7.7	36	1	PCDFY	pancreatic peptide
659	3	7.7	36	1	PCGS	pancreatic hormone
660	3	7.7	36	1	CKAODP	cecropin D - Chine
661	3	7.7	36	2	F22102	phycoerythrin-545
662	3	7.7	36	2	S21276	glutathione transf
663	3	7.7	36	2	PT0430	leucyl aminopeptid
664	3	7.7	36	2	JQ0365	pancreatic hormone
665	3	7.7	36	2	S07052	neuropeptide Y - s
666	3	7.7	36	2	A30485	neuropeptide Y - r
667	3	7.7	36	2	A28578	pancreatic hormone
668	3	7.7	36	2	B30485	neuropeptide Y - g
669	3	7.7	36	2	A48540	neuropeptide Y - c
670	3	7.7	36	2	A39393	neuropeptide Y - l
671	3	7.7	36	2	A49743	pancreatic peptide
672	3	7.7	36	2	A26377	pancreatic peptide
673	3	7.7	36	2	S27054	neuropeptide Y - A
674	3	7.7	36	2	A59064	egg-laying hormone
675	3	7.7	36	2	F42753	interferon alpha (
676	3	7.7	36	2	JH0721	Ig heavy chain V r
677	3	7.7	36	2	JH0722	Ig H chain V regio
678	3	7.7	36	2	JH0723	Ig heavy chain V r
679	3	7.7	36	2	JH0737	Ig heavy chain V r
680	3	7.7	36	2	PH1753	Ig heavy chain V r
681	3	7.7	36	2	C45875	M1 class I histoco
682	3	7.7	36	2	A29164	cartilage proteogl
683	3	7.7	36	2	S07622	avenin gamma-4 - s
684	3	7.7	36	2	A45798	phosphocarrier pro
685	3	7.7	36	2	B41481	virulence-associat
686	3	7.7	36	2	S00317	photosystem I 11K
687	3	7.7	36	2	S00314	photosystem I chai
688	3	7.7	36	2	A60146	65K heat shock pro
689	3	7.7	36	2	A28503	neuropeptide H - b
690	3	7.7	36	2	S73127	hypothetical prote
691	3	7.7	36	2	S78239	ycf32 protein - Od
692	3	7.7	36	2	T06901	hypothetical prote
693	3	7.7	36	2	H48110	RNA recognition mo
694	3	7.7	36	2	B95156	hypothetical prote
695	3	7.7	36	2	F84791	hypothetical prote
696	3	7.7	36	2	D84275	hypothetical prote
697	3	7.7	36	2	S17834	acetyl-CoA carboxy

698	3	7.7	36	2	E70220	hypothetical prote
699	3	7.7	36	2	H70251	hypothetical prote
700	3	7.7	36	2	A64540	hypothetical prote
701	3	7.7	36	2	F64604	hypothetical prote
702	3	7.7	36	2	T44548	hypothetical prote
703	3	7.7	36	2	A81164	hypothetical prote
704	3	7.7	36	2	S16552	hypothetical prote
705	3	7.7	36	2	G82263	hypothetical prote
706	3	7.7	36	2	B82111	hypothetical prote
707	3	7.7	36	2	D82108	hypothetical prote
708	3	7.7	36	2	G82085	hypothetical prote
709	3	7.7	36	2	D82482	hypothetical prote
710	3	7.7	36	2	D82469	hypothetical prote
711	3	7.7	36	2	D82466	hypothetical prote
712	3	7.7	36	2	D82457	hypothetical prote
713	3	7.7	36	2	A82437	hypothetical prote
714	3	7.7	36	2	E69729	required for trans
715	3	7.7	36	2	S70092	hypothetical prote
716	3	7.7	36	2	S42591	dnaA protein - Str
717	3	7.7	36	2	A69287	hypothetical prote
718	3	7.7	36	2	JA0173	basic peptide - wi
719	3	7.7	36	2	T50336	ribosomal protein
720	3	7.7	36	2	S67795	probable membrane
721	3	7.7	36	2	S78721	protein YGL006w-a
722	3	7.7	36	2	B49139	allergen TBA-1 - T
723	3	7.7	36	2	A61235	fibroblast-activat
724	3	7.7	36	2	B53480	T-cell receptor al
725	3	7.7	36	2	A81740	hypothetical prote
726	3	7.7	36	2	G81734	hypothetical prote
727	3	7.7	36	2	H71293	hypothetical prote
728	3	7.7	36	2	E82854	hypothetical prote
729	3	7.7	36	2	H82703	hypothetical prote
730	3	7.7	36	2	C82694	hypothetical prote
731	3	7.7	36	2	D82617	hypothetical prote
732	3	7.7	36	2	A82598	hypothetical prote
733	3	7.7	36	2	C85910	unknown protein en
734	3	7.7	36	2	AH0066	hypothetical prote
735	3	7.7	36	2	A81309	small hydrophobic
736	3	7.7	36	2	AI1841	hypothetical prote
737	3	7.7	37	1	R5PM81	ribosomal protein
738	3	7.7	37	1	R5EG36	ribosomal protein
739	3	7.7	37	1	R5IT36	ribosomal protein
740	3	7.7	37	1	FDFL3W	antifreeze protein
741	3	7.7	37	1	ZJBPF4	gene J protein - p
742	3	7.7	37	1	WRBP65	early protein gp5
743	3	7.7	37	1	WRBPF7	early protein gp5
744	3	7.7	37	2	S73239	plastoquinol-plast
745	3	7.7	37	2	S74215	NADH2 dehydrogenas
746	3	7.7	37	2	S03941	hydrogen dehydroge
747	3	7.7	37	2	S48656	fusicoccin recepto
748	3	7.7	37	2	S03570	trypsin (EC 3.4.21
749	3	7.7	37	2	S02176	acrosin (EC 3.4.21
750	3	7.7	37	2	B38230	inorganic diphosph
751	3	7.7	37	2	A32000	somatostatin, panc
752	3	7.7	37	2	C60580	growth hormone-rel
753	3	7.7	37	2	S26954	peptide YY-related
754	3	7.7	37	2	C32021	bactericidin B-4 -

755	3	7.7	37	2	A32021	bactericidin B-2 -
756	3	7.7	37	2	B32021	bactericidin B-3 -
757	3	7.7	37	2	JH0357	T-cell receptor be
758	3	7.7	37	2	JH0727	Ig heavy chain V r
759	3	7.7	37	2	JH0728	Ig heavy chain V r
760	3	7.7	37	2	JH0729	Ig heavy chain V r
761	3	7.7	37	2	JH0730	Ig heavy chain V r
762	3	7.7	37	2	JH0731	Ig heavy chain V r
763	3	7.7	37	2	JH0734	Ig heavy chain V r
764	3	7.7	37	2	JH0735	Ig heavy chain V r
765	3	7.7	37	2	JH0736	Ig heavy chain V r
766	3	7.7	37	2	JH0738	Ig heavy chain V r
767	3	7.7	37	2	JH0743	Ig heavy chain V r
768	3	7.7	37	2	JH0746	Ig heavy chain V r
769	3	7.7	37	2	JH0747	Ig heavy chain V r
770	3	7.7	37	2	A30607	Ig kappa chain V-I
771	3	7.7	37	2	PS0130	H-2 class I histoc
772	3	7.7	37	2	PS0127	H-2 class I histoc
773	3	7.7	37	2	I48405	histone H2a - mous
774	3	7.7	37	2	S73217	ribosomal protein
775	3	7.7	37	2	B70566	probable ribosomal
776	3	7.7	37	2	E75312	ribosomal protein
777	3	7.7	37	2	T35555	ribosomal protein
778	3	7.7	37	2	D87154	50S ribosomal prot
779	3	7.7	37	2	A57497	agrin-related prot
780	3	7.7	37	2	I51251	myosin heavy chain
781	3	7.7	37	2	I46594	myosin - pig (frag
782	3	7.7	37	2	PC1121	antifungal 25K pro
783	3	7.7	37	2	S17684	thaumatin homolog
784	3	7.7	37	2	A57222	phosphocarrier pro
785	3	7.7	37	2	PS0187	photosystem II oxy
786	3	7.7	37	2	JN0035	early protein gp5
787	3	7.7	37	2	D47099	hypothetical prote
788	3	7.7	37	2	T07292	hypothetical prote
789	3	7.7	37	2	G45187	homeotic protein G
790	3	7.7	37	2	F45187	homeotic protein G
791	3	7.7	37	2	F90765	hypothetical prote
792	3	7.7	37	2	E87618	hypothetical prote
793	3	7.7	37	2	G84233	hypothetical prote
794	3	7.7	37	2	D84284	hypothetical prote
795	3	7.7	37	2	S07517	gene 6.3 protein -
796	3	7.7	37	2	E70241	hypothetical prote
797	3	7.7	37	2	C36727	cytochrome c552 -
798	3	7.7	37	2	S54441	hypothetical prote
799	3	7.7	37	2	C82364	hypothetical prote
800	3	7.7	37	2	H82319	hypothetical prote
801	3	7.7	37	2	A82439	hypothetical prote
802	3	7.7	37	2	B36511	hypothetical prote
803	3	7.7	37	2	S21132	photosystem II cyt
804	3	7.7	37	2	I40568	rap60 regulator ra
805	3	7.7	37	2	S50905	fatty acid beta-ox
806	3	7.7	37	2	T48964	hypothetical prote
807	3	7.7	37	2	T06571	hypothetical prote
808	3	7.7	37	2	S03432	hypothetical prote
809	3	7.7	37	2	A45609	calcium-binding pr
810	3	7.7	37	2	C41933	mating pheromone E
811	3	7.7	37	2	T29808	hypothetical prote

812	3	7.7	37	2	T20564	hypothetical prote
813	3	7.7	37	2	B60529	hemocyanin 4 - edi
814	3	7.7	37	2	S14101	apolipophorin III
815	3	7.7	37	2	A61438	receptor binding f
816	3	7.7	37	2	C32112	R15 gamma peptide
817	3	7.7	37	2	S03837	hcr protein - wood
818	3	7.7	37	2	I49615	gamma-D-crystallin
819	3	7.7	37	2	B39030	androgen-binding p
820	3	7.7	37	2	E83665	hypothetical prote
821	3	7.7	37	2	C83780	hypothetical prote
822	3	7.7	37	2	A81552	hypothetical prote
823	3	7.7	37	2	E81738	hypothetical prote
824	3	7.7	37	2	B85574	hypothetical prote
825	3	7.7	37	2	H85612	hypothetical prote
826	3	7.7	37	2	G95919	probable transposa
827	3	7.7	37	2	AH0455	hypothetical prote
828	3	7.7	37	2	S70931	histone-like prote
829	3	7.7	37	2	AB0592	probable membrane
830	3	7.7	37	2	AH0637	conserved hypothet
831	3	7.7	37	2	AH0844	hypothetical prote
832	3	7.7	37	2	E97596	hypothetical prote
833	3	7.7	37	4	JE0019	probable 4K protei
834	3	7.7	38	1	HWGHS	exendin-1 - Mexica
835	3	7.7	38	2	S04627	glutathione transf
836	3	7.7	38	2	C34047	stylar glycoprotei
837	3	7.7	38	2	A05222	anthranilate phosp
838	3	7.7	38	2	S39034	lipid transfer pro
839	3	7.7	38	2	A49165	pituitary adenyлат
840	3	7.7	38	2	A61070	pituitary adenyлат
841	3	7.7	38	2	JH0724	Ig heavy chain V r
842	3	7.7	38	2	JH0725	Ig heavy chain V r
843	3	7.7	38	2	PS0115	H-2 class I histoc
844	3	7.7	38	2	I58994	MHC H2-L transmemb
845	3	7.7	38	2	S12409	ribosomal protein
846	3	7.7	38	2	S07140	ribosomal protein
847	3	7.7	38	2	I46861	macrophage migrati
848	3	7.7	38	2	I65220	dopamine D3 recept
849	3	7.7	38	2	I64844	SP-A1 (gamma, delt
850	3	7.7	38	2	PH0104	integrin beta 1 ch
851	3	7.7	38	2	T12207	chaperonin homolog
852	3	7.7	38	2	S78349	photosystem I prot
853	3	7.7	38	2	A59185	photosystem II pro
854	3	7.7	38	2	G45095	photosystem I ligh
855	3	7.7	38	2	JS0456	gene J protein - p
856	3	7.7	38	2	B53708	indolepyruvate syn
857	3	7.7	38	2	A37902	myotrophin - rat (
858	3	7.7	38	2	H95005	hypothetical prote
859	3	7.7	38	2	B95069	hypothetical prote
860	3	7.7	38	2	H91111	hypothetical prote
861	3	7.7	38	2	S07972	regulatory protein
862	3	7.7	38	2	E72306	hypothetical prote
863	3	7.7	38	2	D55543	Tnp protein - Pseu
864	3	7.7	38	2	G81904	hypothetical prote
865	3	7.7	38	2	C81171	hypothetical prote
866	3	7.7	38	2	A47307	heat-stable entero
867	3	7.7	38	2	D82121	hypothetical prote
868	3	7.7	38	2	D82115	hypothetical prote

869	3	7.7	38	2	F82485	hypothetical prote
870	3	7.7	38	2	C82482	hypothetical prote
871	3	7.7	38	2	G64001	hypothetical prote
872	3	7.7	38	2	T36775	hypothetical prote
873	3	7.7	38	2	T37138	hypothetical prote
874	3	7.7	38	2	S61280	nikkomycin synthet
875	3	7.7	38	2	S78357	photosystem II pro
876	3	7.7	38	2	JN0418	hypothetical prote
877	3	7.7	38	2	S55678	calcium-dependent
878	3	7.7	38	2	S14141	hypothetical prote
879	3	7.7	38	2	T04074	transcription acti
880	3	7.7	38	2	T01741	hypothetical prote
881	3	7.7	38	2	S39376	lectin - shallot
882	3	7.7	38	2	S78728	protein YLR264c-a
883	3	7.7	38	2	T15508	hypothetical prote
884	3	7.7	38	2	T34310	hypothetical prote
885	3	7.7	38	2	A32112	R15 alpha 1 osmore
886	3	7.7	38	2	S78757	ribosomal protein
887	3	7.7	38	2	C83729	hypothetical prote
888	3	7.7	38	2	H81603	hypothetical prote
889	3	7.7	38	2	E82858	hypothetical prote
890	3	7.7	38	2	T46593	phytoene dehydroge
891	3	7.7	38	2	A97169	hypothetical prote
892	3	7.7	38	2	E89922	hypothetical prote
893	3	7.7	38	2	T08652	hypothetical prote
894	3	7.7	38	2	AB0747	hypothetical prote
895	3	7.7	38	2	AD0740	hypothetical prote
896	3	7.7	38	2	C97551	hypothetical prote
897	3	7.7	39	1	S28546	protamine 1 - Japa
898	3	7.7	39	1	C69677	phosphatase (RapF)
899	3	7.7	39	2	S65949	hypothetical prote
900	3	7.7	39	2	S33872	glyceraldehyde-3-p
901	3	7.7	39	2	I46149	aldolase A - dog (
902	3	7.7	39	2	I57685	aldolase A - south
903	3	7.7	39	2	S00490	RNA-binding protei
904	3	7.7	39	2	S54330	trypsin inhibitor
905	3	7.7	39	2	I49418	insulin I precurso
906	3	7.7	39	2	D42753	interferon alpha (
907	3	7.7	39	2	E30517	Ig heavy chain pre
908	3	7.7	39	2	PH0878	Ig kappa chain V r
909	3	7.7	39	2	A32934	H-2 class I-like h
910	3	7.7	39	2	S01813	hemoglobin BI - tu
911	3	7.7	39	2	S68791	ribosomal protein
912	3	7.7	39	2	A45479	GTP-binding regula
913	3	7.7	39	2	A38673	G protein alpha i-
914	3	7.7	39	2	A05331	colipase - spiny d
915	3	7.7	39	2	S23804	homeotic protein 1
916	3	7.7	39	2	A03353	glutenin 2 - wheat
917	3	7.7	39	2	A54531	circumsporozoite a
918	3	7.7	39	2	E42799	photosystem I chai
919	3	7.7	39	2	S10315	photosystem II pro
920	3	7.7	39	2	S75180	photosystem II pro
921	3	7.7	39	2	AH2286	photosystem II pro
922	3	7.7	39	2	A33975	gag polyprotein -
923	3	7.7	39	2	S77904	tax protein - simi
924	3	7.7	39	2	PS0063	lysis protein t -
925	3	7.7	39	2	G64944	yebJ protein - Esc

926	3	7.7	39	2	A85795	hypothetical prote
927	3	7.7	39	2	S19540	isocitrate dehydro
928	3	7.7	39	2	S78008	fucosyltransferase
929	3	7.7	39	2	S18569	hypothetical prote
930	3	7.7	39	2	S22880	gonadal protein gd
931	3	7.7	39	2	I65265	homeotic protein H
932	3	7.7	39	2	I38143	homeobox - human (
933	3	7.7	39	2	S35325	protein kinase sgg
934	3	7.7	39	2	H95135	hypothetical prote
935	3	7.7	39	2	G90716	probable RNA [impo
936	3	7.7	39	2	C87422	hypothetical prote
937	3	7.7	39	2	C84197	anthranilate synth
938	3	7.7	39	2	G70228	hypothetical prote
939	3	7.7	39	2	B64559	hypothetical prote
940	3	7.7	39	2	G83252	hypothetical prote
941	3	7.7	39	2	E81920	hypothetical prote
942	3	7.7	39	2	A81151	hypothetical prote
943	3	7.7	39	2	A82359	hypothetical prote
944	3	7.7	39	2	H82310	hypothetical prote
945	3	7.7	39	2	G82287	hypothetical prote
946	3	7.7	39	2	F82226	hypothetical prote
947	3	7.7	39	2	B82419	hypothetical prote
948	3	7.7	39	2	S75759	hypothetical prote
949	3	7.7	39	2	S74393	photosystem II Psb
950	3	7.7	39	2	T06940	photosystem II pro
951	3	7.7	39	2	S73118	photosystem II pro
952	3	7.7	39	2	T15158	hypothetical prote
953	3	7.7	39	2	S23803	homeotic protein l
954	3	7.7	39	2	S48644	oxidase - Malayan
955	3	7.7	39	2	I37555	homeobox - human (
956	3	7.7	39	2	I37556	homeobox - human (
957	3	7.7	39	2	S28908	dynein-associated
958	3	7.7	39	2	I46466	luteinizing hormon
959	3	7.7	39	2	D40984	finger protein zfa
960	3	7.7	39	2	B40984	finger protein zfe
961	3	7.7	39	2	I65323	calpain II - rat (
962	3	7.7	39	2	G83716	hypothetical prote
963	3	7.7	39	2	D83721	hypothetical prote
964	3	7.7	39	2	C83904	hypothetical prote
965	3	7.7	39	2	E81540	hypothetical prote
966	3	7.7	39	2	B71285	hypothetical prote
967	3	7.7	39	2	G82733	hypothetical prote
968	3	7.7	39	2	G82718	hypothetical prote
969	3	7.7	39	2	A82707	hypothetical prote
970	3	7.7	39	2	G82619	hypothetical prote
971	3	7.7	39	2	B85609	hypothetical prote
972	3	7.7	39	2	B85990	hypothetical prote
973	3	7.7	39	2	D85649	hypothetical prote
974	3	7.7	39	2	F97313	hypothetical prote
975	3	7.7	39	2	A96026	probable transposa
976	3	7.7	39	2	AC0205	hypothetical prote
977	3	7.7	39	2	F64843	hypothetical prote
978	3	7.7	39	2	G64801	hypothetical prote
979	3	7.7	39	2	AE3109	hypothetical prote
980	3	7.7	39	2	C97513	hypothetical prote
981	3	7.7	39	2	AB1924	photosystem II pro
982	3	7.7	39	2	AB2010	hypothetical prote

983	3	7.7	39	2	AB2552	hypothetical prote
984	3	7.7	40	1	SWFGS	sauvagine - Sauvag
985	3	7.7	40	1	S14717	protamine 2 - Japa
986	3	7.7	40	1	FDFI8G	antifreeze protein
987	3	7.7	40	1	W4BP17	gene 4.1 protein -
988	3	7.7	40	1	A69677	phosphatase (RapC)
989	3	7.7	40	2	S09338	ferredoxin [2Fe-2S
990	3	7.7	40	2	E61320	plastocyanin - Era
991	3	7.7	40	2	E22565	R-phycoerythrin be
992	3	7.7	40	2	B27398	allophycocyanin al
993	3	7.7	40	2	T05931	probable 5-methylt
994	3	7.7	40	2	PQ0533	3-oxoacyl-[acyl-ca
995	3	7.7	40	2	JH0756	sucrose-specific e
996	3	7.7	40	2	A29502	carboxylesterase (
997	3	7.7	40	2	S50021	trypsin-like prote
998	3	7.7	40	2	A49081	capillary permeabi
999	3	7.7	40	2	B41440	protein disulfide-
1000	3	7.7	40	2	S29489	GTP-binding protei

ALIGNMENTS

RESULT 1

G83440

KdpF protein PA1632 [imported] - Pseudomonas aeruginosa (strain PA01)
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: G83440
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brinkman, F.S.L.; Hufnagle, W.O.; Kowalik, D.J.; Lagrou, M.; Garber, R.L.; Goltry, L.; Tolentino, E.; Westbrook-Wadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, R.M.; Smith, K.A.; Spencer, D.H.; Wong, G.K.S.; Wu, Z.; Paulsen, I.T.; Reizer, J.; Saier, M.H.; Hancock, R.E.W.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen.
 A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Accession: G83440
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-29 <STO>
 A;Cross-references: GB:AE004591; GB:AE004091; NID:g9947599; PIDN:AAG05021.1; GSPDB:GN00131; PASP:PA1632
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: kdpF; PA1632

Query Match 12.8%; Score 5; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 SLALA 5
Db	8 SLALA 12

RESULT 2
A32860
biotin-binding protein I - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 24-Jun-1993
C;Accession: A32860
R;Bush, L.; White III, H.B.
J. Biol. Chem. 264, 5741-5745, 1989
A;Title: Conversion of domains into subunits in the processing of egg yolk biotin-binding protein I.
A;Reference number: A32860; MUID:89174628; PMID:2925632
A;Accession: A32860
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-29 <BUS>

Query Match 12.8%; Score 5; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ALADD 7
| | | |
Db 23 ALADD 27

RESULT 3
S05124
hypothetical protein 31 - rice chloroplast
C;Species: chloroplast Oryza sativa (rice)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jul-2000
C;Accession: S05124
R;Hiratsuka, J.; Shimada, H.; Whittier, R.; Ishibashi, T.; Sakamoto, M.; Mori, M.; Kondo, C.; Honji, Y.; Sun, C.R.; Meng, B.Y.; Li, Y.Q.; Kanno, A.; Nishizawa, Y.; Hirai, A.; Shinozaki, K.; Sugiura, M.
Mol. Gen. Genet. 217, 185-194, 1989
A;Title: The complete sequence of the rice (*Oryza sativa*) chloroplast genome: intermolecular recombination between distinct tRNA genes accounts for a major plastid DNA inversion during the evolution of the cereals.
A;Reference number: S05080; MUID:89364698; PMID:2770692
A;Accession: S05124
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-31 <HIR>
A;Cross-references: EMBL:X15901; NID:g11957; PIDN:CAA33966.1; PID:g12005
A;Note: this sequence was submitted to the EMBL Data Library, July 1989
C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast

Query Match 12.8%; Score 5; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLAAL 20
| | | |
Db 11 LLAAL 15

RESULT 4

S58569

hypothetical protein 31 - maize chloroplast

C;Species: chloroplast Zea mays (maize)

C;Date: 29-Nov-1995 #sequence_revision 19-Jan-1996 #text_change 29-Oct-1999

C;Accession: S58569

R;Maier, R.M.; Neckermann, K.; Igloi, G.L.; Koessel, H.

J. Mol. Biol. 251, 614-628, 1995

A;Title: Complete sequence of the maize chloroplast genome: gene content, hotspots of divergence and fine tuning of genetic information by transcript editing.

A;Reference number: S58531; MUID:95395841; PMID:7666415

A;Accession: S58569

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-31 <MAI>

A;Cross-references: EMBL:X86563; NID:g902200; PIDN:CAA60303.1; PID:g902239

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995

C;Genetics:

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match 12.8%; Score 5; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20

|||||

Db 11 LLAAL 15

RESULT 5

T14568

hypothetical protein ycf7 - beet chloroplast

C;Species: chloroplast Beta vulgaris (beet)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C;Accession: T14568

R;Ran, Z.; Michaelis, G.

Theor. Appl. Genet. 91, 836-840, 1995

A;Title: Mapping of a chloroplast RFLP marker associated with the CMS cytoplasm of sugar beet (Beta vulgaris).

A;Reference number: Z18144

A;Accession: T14568

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-31 <RAN>

A;Cross-references: EMBL:X87636; NID:g860887; PID:g860889

C;Genetics:

A;Genome: chloroplast

A;Note: ycf7

C;Keywords: chloroplast

Query Match 12.8%; Score 5; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 16 LLAAL 20
|||||
Db 11 LIAAL 15

RESULT 6

A82451

hypothetical protein VCA0500 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: A82451

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill, S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.; Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.; Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: A82451

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-33 <HEI>

A;Cross-references: GB:AE004381; GB:AE003853; NID:g9657902; PIDN:AAF96403.1; GSPDB:GN00127; TIGR:VCA0500

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VCA0500

A;Map position: 2

Query Match 12.8%; Score 5; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 DDAAF 10
|||||
Db 16 DDAAF 20

RESULT 7

G97576

hypothetical protein AGR_C_3308 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)

C;Species: Agrobacterium tumefaciens

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002

C;Accession: G97576

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quroollo, B.; Goldman, B.S.; Cao, Y.; Askenazi, M.; Halling, C.; Mullin, L.; Houmiel, K.; Gordon, J.; Vaudin, M.; Iartchouk, O.; Epp, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Flanagan, C.; Crowell, C.; Gurson, J.; Lomo, C.; Sear, C.; Strub, G.; Cielo, C.; Slater, S.

Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent
Agrobacterium tumefaciens C58.
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: G97576
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-38 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK87568.1; PID:g15156908; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_3308
A;Map position: circular chromosome

Query Match 12.8%; Score 5; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 KLLVL 36
| ||||
Db 16 KLLVL 20

RESULT 8
T14210
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Uromastyx acanthinurus
mitochondrion (fragment)
C;Species: mitochondrion Uromastyx acanthinurus
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C;Accession: T14210
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A;Title: Two novel gene orders and the role of light-strand replication in
rearrangement of the vertebrate mitochondrial genome.
A;Reference number: Z17789; MUID:97153826; PMID:9000757
A;Accession: T14210
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-28 <MAC>
A;Cross-references: EMBL:U71325; NID:g1753264; PID:g1753265; PIDN: AAC62247.1
A;Experimental source: specimen voucher MVZ162567; Museum of Vertebrate Zoology,
University of California at Berkeley
C;Genetics:
A;Genome: mitochondrion
A;Note: ND1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative
phosphorylation; oxidoreductase; respiratory chain

Query Match 10.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LAAL 20
| |||
Db 20 LAAL 23

RESULT 9

S21278
glutathione transferase (EC 2.5.1.18) alpha-Yx - rat (fragment)
N;Alternate names: glutathione S-transferase Yx; glutathione transferase Yfetus
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
C;Accession: S21278
R;Igarashi, T.; Tsuchiya, T.; Shikata, Y.; Sagami, F.; Tagaya, O.; Horie, T.;
Satoh, T.
Biochem. J. 283, 307-311, 1992
A;Title: Developmental aspects of a unique glutathione S-transferase subunit Yx
in the liver cytosol from rats with hereditary hyperbilirubinuria. Comparison
with rat fetal liver transferase subunit Yfetus.
A;Reference number: S21278; MUID:92231842; PMID:1567376
A;Accession: S21278
A;Molecule type: protein
A;Residues: 1-28 <IGA>
C;Superfamily: glutathione transferase
C;Keywords: dimer; liver; transferase

Query Match 10.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAA 19
| |||
Db 21 LLAA 24

RESULT 10
B35948
phospholipase A2 (EC 3.1.1.4) 2 - black-banded coral snake (fragment)
C;Species: Micrurus nigrocinctus (black-banded coral snake)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 12-Apr-1995
C;Accession: B35948
R;Mochca-Morales, J.; Martin, B.M.; Zamudio, F.Z.; Possani, L.D.
Toxicon 28, 616-617, 1990
A;Title: Isolation and characterization of three toxic phospholipases from the
venom of the coral snake *Micrurus nigrocinctus*.
A;Reference number: A35948
A;Accession: B35948
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <MOC>
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase

Query Match 10.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 RHWL 26
| |||
Db 15 RHWL 18

RESULT 11
A56366

intestinal trefoil factor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: A56366
R;Sands, B.E.; Ogata, H.; Lynch-Devaney, K.; deBeaumont, M.; Ezzell, R.M.;
Podolsky, D.K.
J. Biol. Chem. 270, 9353-9361, 1995
A;Title: Molecular cloning of the rat intestinal trefoil factor gene.
Characterization of an intestinal goblet cell-associated promoter.
A;Reference number: A56366; MUID:95238450; PMID:7721858
A;Accession: A56366
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-28 <RES>
A;Cross-references: EMBL:U20984; NID:g930338; PIDN:AAB01063.1; PID:g930339
C;Superfamily: secretory protein xP1; trefoil homology
C;Keywords: intestine

Query Match 10.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 LLVL 36
|||
Db 11 LLVL 14

RESULT 12
PH0231
T-cell receptor Vb CDR3, carrier PBL Vb 6.sbt - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 30-May-1997
C;Accession: PH0231
R;Hara, H.; Morita, M.; Iwaki, T.; Hatae, T.; Itoyama, Y.; Kitamoto, T.;
Akizuki, S.; Goto, I.; Watanabe, T.
submitted to JIPID, June 1994
A;Description: Detection of HTLV-I proviral DNA and analysis of T cell receptor
Vb CDR3 sequences in spinal cord lesions of HTLV-I associated
myelopathy/Tropical spastic paraparesis.
A;Reference number: PH0227
A;Accession: PH0231
A;Molecule type: mRNA
A;Residues: 1-28 <HAR>
A;Experimental source: spinal cord
C;Genetics:
A;Map position: 7
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: receptor

Query Match 10.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 LLVL 36
|||
Db 20 LLVL 23

RESULT 13

T06925

hypothetical protein L - Cyanophora paradoxa cyanelle

C;Species: cyanelle Cyanophora paradoxa

C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999

C;Accession: T06925

R;Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.

submitted to the EMBL Data Library, July 1995

A;Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.

A;Reference number: Z15840

A;Accession: T06925

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-28 <STI>

A;Cross-references: EMBL:U30821; NID:g1016083; PIDN:AAA81268.1; PID:g1016181

A;Experimental source: strain Pringsheim LB55

C;Genetics:

A;Gene: petL

A;Genome: cyanelle

C;Keywords: cyanelle

Query Match 10.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
|||
Db 14 LALA 17

RESULT 14

JQ1035

hypothetical 3.2K protein (type I IGFR 5' region) - human

C;Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C;Accession: JQ1035

R;Cooke, D.W.; Bankert, L.A.; Roberts Jr., C.T.; LeRoith, D.; Casella, S.J.
Biochem. Biophys. Res. Commun. 177, 1113-1120, 1991

A;Title: Analysis of the human type I insulin-like growth factor receptor promotor region.

A;Reference number: PQ0159; MUID:91282751; PMID:1711844

A;Accession: JQ1035

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <COO>

Query Match 10.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ADDA 8
|||
Db 3 ADDA 6

RESULT 15
E47719
house-dust-mite-reactive T-cell receptor beta chain (CD4+ clone DE26, V(D)J
junctional region) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C;Accession: E47719
R;Wedderburn, L.R.; O'Hehir, R.E.; Hewitt, C.R.; Lamb, J.R.; Owen, M.J.
Proc. Natl. Acad. Sci. U.S.A. 90, 8214-8218, 1993
A;Title: In vivo clonal dominance and limited T-cell receptor usage in human
CD4+ T-cell recognition of house dust mite allergens.
A;Reference number: A47719; MUID:93376774; PMID:8367485
A;Accession: E47719
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-29 <WED>
A;Note: sequence extracted from NCBI backbone (NCBIN:137825, NCBIP:137831)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 LLVL 36
|||
Db 22 LLVL 25

RESULT 16
S58390
T-cell receptor beta-chain Vb6-Jb2.5 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 23-Jul-1999
C;Accession: S58390
R;Johnston, S.L.; Strausbauch, M.; Sarkar, G.; Wettstein, P.J.
Nucleic Acids Res. 23, 3074-3075, 1995
A;Title: A novel method for sequencing members of multi-gene families.
A;Reference number: S58384; MUID:95388532; PMID:7659534
A;Accession: S58390
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-29 <JOH>
A;Cross-references: EMBL:U20304; NID:g663131; PIDN:AAA62251.1; PID:g663132
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January
1995
A;Note: only a part of the coding sequence is given
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 LLVL 36
|||

Db 26 LLVL 29

RESULT 17

I37534

gene HLA-DRB protein - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 23-Jul-1999

C;Accession: I37534

R;Louis, P.; Eliaou, J.F.; Kerlan-Candon, S.; Pinet, V.; Vincent, R.; Clot, J.
Immunogenetics 38, 21-26, 1993

A;Title: Polymorphism in the regulatory region of HLA-DRB genes correlating with
haplotype evolution.

A;Reference number: I37300; MUID:93216303; PMID:8462990

A;Accession: I37534

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RES>

A;Cross-references: EMBL:X65585; NID:g296296; PIDN:CAA46544.1; PID:g296297

C;Genetics:

A;Gene: HLA-DRB

C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
||||

Db 26 LALA 29

RESULT 18

I37535

gene HLA-DRB protein - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 23-Jul-1999

C;Accession: I37535

R;Louis, P.; Eliaou, J.F.; Kerlan-Candon, S.; Pinet, V.; Vincent, R.; Clot, J.
Immunogenetics 38, 21-26, 1993

A;Title: Polymorphism in the regulatory region of HLA-DRB genes correlating with
haplotype evolution.

A;Reference number: I37300; MUID:93216303; PMID:8462990

A;Accession: I37535

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RES>

A;Cross-references: EMBL:X65586; NID:g296298; PIDN:CAA46545.1; PID:g296299

C;Genetics:

A;Gene: HLA-DRB

C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5

Db ||||
26 LALA 29

RESULT 19

I37536

MHC class II histocompatibility antigen HLA-DRB1*0401 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 23-Jul-1999

C;Accession: I37536

R;Louis, P.; Eliaou, J.F.; Kerlan-Candon, S.; Pinet, V.; Vincent, R.; Clot, J.
Immunogenetics 38, 21-26, 1993

A;Title: Polymorphism in the regulatory region of HLA-DRB genes correlating with
haplotype evolution.

A;Reference number: I37300; MUID:93216303; PMID:8462990

A;Accession: I37536

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RES>

A;Cross-references: EMBL:X65587; NID:g296300; PIDN:CAA46546.1; PID:g296301

C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LALA 5
 ||||
Db 26 LALA 29

RESULT 20

I37301

MHC class II histocompatibility antigen HLA-DR beta-3 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999

C;Accession: I37301; I37302

R;Louis, P.; Eliaou, J.F.; Kerlan-Candon, S.; Pinet, V.; Vincent, R.; Clot, J.
Immunogenetics 38, 21-26, 1993

A;Title: Polymorphism in the regulatory region of HLA-DRB genes correlating with
haplotype evolution.

A;Reference number: I37300; MUID:93216303; PMID:8462990

A;Accession: I37301

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RES>

A;Cross-references: EMBL:X65558; NID:g296268; PIDN:CAA46528.1; PID:g296269

A;Note: this allele is designated DRB3*0101

A;Accession: I37302

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RE2>

A;Cross-references: EMBL:X65559; NID:g296270; PIDN:CAA46529.1; PID:g296271

A;Note: this allele is designated DRB3*0201

C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 10.3%; Score 4; DB 2; Length 29;

Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20

||||

Db 12 LAAL 15

RESULT 21

I37303

HLA-DR beta - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999

C;Accession: I37303; I37305

R;Louis, P.; Eliaou, J.F.; Kerlan-Candon, S.; Pinet, V.; Vincent, R.; Clot, J.
Immunogenetics 38, 21-26, 1993

A;Title: Polymorphism in the regulatory region of HLA-DRB genes correlating with
haplotype evolution.

A;Reference number: I37300; MUID:93216303; PMID:8462990

A;Accession: I37303

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RES>

A;Cross-references: EMBL:X64544; NID:g296276; PIDN:CAA45842.1; PID:g296277

A;Accession: I37305

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RE2>

A;Cross-references: EMBL:X64548; NID:g296280; PIDN:CAA45846.1; PID:g296281

C;Genetics:

A;Gene: GDB:HLA-DRB5

A;Cross-references: GDB:125658

A;Map position: 6p21.3-6p21.3

C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 10.3%; Score 4; DB 2; Length 29;

Best Local Similarity 100.0%; Pred. No. 3.3e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5

||||

Db 26 LALA 29

RESULT 22

I37306

HLA-DR beta - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999

C;Accession: I37306

R;Louis, P.; Eliaou, J.F.; Kerlan-Candon, S.; Pinet, V.; Vincent, R.; Clot, J.
Immunogenetics 38, 21-26, 1993

A;Title: Polymorphism in the regulatory region of HLA-DRB genes correlating with
haplotype evolution.

A;Reference number: I37300; MUID:93216303; PMID:8462990

A;Accession: I37306

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-29 <RES>
A;Cross-references: EMBL:X64549; NID:g296282; PIDN:CAA45847.1; PID:g296283
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
|||
Db 26 LALA 29

RESULT 23

S78326
conserved hypothetical protein 29 - Odontella sinensis chloroplast
C;Species: chloroplast Odontella sinensis
C;Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 24-Apr-1998
C;Accession: S78326
R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
Plant Mol. Biol. Rep. 13, 336-342, 1995
A;Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella
sinensis.
A;Reference number: S78238
A;Accession: S78326
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-29 <KOW>
A;Cross-references: EMBL:Z67753; NID:g1185127; PID:e211871; PID:g1185216
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November
1995
C;Genetics:
A;Gene: ycf6
A;Genome: chloroplast
C;Keywords: chloroplast

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLAL 4
|||
Db 18 SLAL 21

RESULT 24

S16323
hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
C;Accession: S16323
R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
EMBO J. 10, 1787-1791, 1991
A;Title: A novel class of plant proteins containing a homeodomain with a closely
linked leucine zipper motif.
A;Reference number: S16323; MUID:91266907; PMID:1675603

A;Accession: S16323
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-29 <RUB>
A;Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41623.1; PID:g16328

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ARLL 17
| |||
Db 13 ARLL 16

RESULT 25

S78714
protein YDR524w-a - yeast (*Saccharomyces cerevisiae*)
C;Species: *Saccharomyces cerevisiae*
C;Date: 15-Jan-1999 #sequence_revision 15-Jan-1999 #text_change 15-Jan-1999

C;Accession: S78714

R;Dietrich, F.S.

submitted to the EMBL Data Library, August 1995

A;Description: The sequence of *S. cerevisiae* cosmids 8166, 9787, 9717, and lambda 3073.

A;Reference number: S69553

A;Accession: S78714

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-29 <DIE>

A;Cross-references: EMBL:U33057; MIPS:YDR524w-a

C;Genetics:

A;Map position: 4R

Query Match 10.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 LLVL 36
| |||
Db 26 LLVL 29

RESULT 26

S21195
spectrin beta chain - pig
C;Species: *Sus scrofa domestica* (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S21195

R;Frappier, T.; Derancourt, J.; Pradel, L.A.

Eur. J. Biochem. 205, 85-91, 1992

A;Title: Actin and neurofilament binding domain of brain spectrin beta subunit.

A;Reference number: S21195; MUID:92209538; PMID:1555607

A;Accession: S21195

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-30 <FRA>

C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology;
spectrin/dystrophin repeat homology; WW repeat homology

Query Match 10.3%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ALAD 6
| || |
Db 1 ALAD 4

RESULT 27

S30333

N-carbamoyl-D-amino acid amidohydrolase (EC 3.5.-.-) - Comamonas sp. (fragment)

C;Species: Comamonas sp.

C;Date: 19-Mar-1997 #sequence_revision 24-Oct-1998 #text_change 26-May-2000

C;Accession: S30333

R;Ogawa, J.; Shimizu, S.; Yamada, H.

Eur. J. Biochem. 212, 685-691, 1993

A;Title: N-carbamoyl-D-amino acid amidohydrolase from Comamonas sp. E222c.

Purification and characterization.

A;Reference number: S30333; MUID:93215645; PMID:8462543

A;Accession: S30333

A;Molecule type: protein

A;Residues: 1-30 <OGA>

A;Experimental source: strain E222c

C;Function:

A;Description: amidohydrolase with strict specificity for the D-form and strict substrate specificity for N-carbamoyl-D-amino acids, no reaction with substrates like N-carbamoyl-beta-alanine or N-carbamoyl-DL-aspartate

C;Superfamily: hypothetical protein YLR351c

C;Keywords: hydrolase

Query Match 10.3%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 RLLA 18
| || |
Db 26 RLLA 29

RESULT 28

E84786

hypothetical protein At2g36940 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: E84786

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84786
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-30 <STO>
A;Cross-references: GB:AE002093; NID:g4883610; PIDN:AAD31579.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g36940
A;Map position: 2

Query Match 10.3%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLAL 4
|||
Db 9 SLAL 12

RESULT 29

PH0236

T-cell receptor Vb CDR3, Ctr2 TCR Vb12 CDR 3aa.sbt - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-May-1997
C;Accession: PH0236
R;Hara, H.; Morita, M.; Iwaki, T.; Hatae, T.; Itoyama, Y.; Kitamoto, T.;
Akizuki, S.; Goto, I.; Watanabe, T.
submitted to JIPID, June 1994

A;Description: Detection of HTLV-I proviral DNA and analysis of T cell receptor Vb CDR3 sequences in spinal cord lesions of HTLV-I associated myelopathy/Tropical spastic paraparesis.

A;Reference number: PH0227

A;Accession: PH0236

A;Molecule type: mRNA

A;Residues: 1-31 <HAR>

A;Experimental source: spinal cord

C;Genetics:

A;Map position: 7

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: receptor

Query Match 10.3%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 LLVL 36
|||
Db 23 LLVL 26

RESULT 30

I48082

mitochondrial benzodiazepine receptor - Chinese hamster (fragment)

C;Species: Cricetulus griseus (Chinese hamster)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999

C;Accession: I48082
R;Yakovlev, A.G.; Ruffo, M.; Jurka, J.; Krueger, K.E.
Gene 155, 201-205, 1995
A;Title: Comparison of repetitive elements in the third intron of human and rodent mitochondrial benzodiazepine receptor-encoding genes.
A;Reference number: I38724; MUID:95237610; PMID:7721091
A;Accession: I48082
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-31 <RES>
A;Cross-references: EMBL:U12420; NID:g529943; PIDN:AAA83251.1; PID:g1039378
C;Genetics:
A;Gene: MBR
A;Introns: 13/3
C;Superfamily: peripheral-type benzodiazepine receptor
C;Keywords: mitochondrion

Query Match 10.3%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ALAD 6
|||
Db 14 ALAD 17

RESULT 31
S76281
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S76281
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76281
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-31 <KAN>
A;Cross-references: EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA10133.1; PID:d1010784; PID:g1673336
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 10.3%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AFRE 12
|||

Db 22 AFRE 25

RESULT 32

S74965

photosystem I reaction center chain psaM - Synechocystis sp. (strain PCC 6803)

N;Alternate names: protein smr0005

C;Species: Synechocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C;Accession: S74965

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirose, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S74965

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-31 <KAN>

A;Cross-references: EMBL:D90902; GB:AB001339; NID:g1652027; PIDN:BAA17005.1; PID:d1017738; PID:g1652080

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Genetics:

A;Gene: psaM

Query Match 10.3%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20

||||

Db 9 LAAL 12

RESULT 33

D82827

hypothetical protein XF0271 [imported] - Xylella fastidiosa (strain 9a5c)

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C;Accession: D82827

R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing and Analysis, Sao Paulo, Brazil.

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: D82827

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-31 <SIM>

A;Cross-references: GB:AE003880; GB:AE003849; NID:g9105080; PIDN:AAF83084.1;
GSPDB:GN00128; XFSC:XF0271

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.;
Alvarenga, R.; Alves, L.M.C.; Araya, J.E.; Baia, G.S.; Baptista, C.S.; Barros,
M.H.; Bonaccorsi, E.D.; Bordin, S.; Bove, J.M.; Briones, M.R.S.; Bueno, M.R.P.;
Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.; Colauto, N.B.;
Colombo, C.; Costa, F.F.; Costa, M.C.R.; Costa-Neto, C.M.; Coutinho, L.L.;
Cristofani, M.; Dias-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.;
Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco,
M.C.; Frohme, M.; Furlan, L.R.; Garnier, M.; Goldman, G.H.; Goldman, M.H.S.;
Gomes, S.L.; Gruber, A.; Ho, P.L.; Hoheisel, J.D.; Junqueira, M.L.; Kemper,
E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigret, F.; Lambais, M.R.;
Leite, L.C.C.; Lemos, E.G.M.; Lemos, M.V.F.; Lopes, S.A.; Lopes, C.R.; Machado,
J.A.; Machado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques,
M.V.; Martins, E.A.L.

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.;
Miyaki, C.Y.; Monteiro-Vitorello, C.B.; Moon, D.H.; Nagai, M.A.; Nascimento,
A.L.T.O.; Netto, L.E.S.; Nhani Jr., A.; Nobrega, F.G.; Nunes, L.R.; Oliveira,
M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Paris, A.; Peixoto,
B.R.; Pereira, G.A.G.; Pereira Jr., H.A.; Pesquero, J.B.; Quaggio, R.B.;
Roberto, P.G.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.;
Santelli, R.V.; Sawasaki, H.E.

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da
Silveira, J.F.; Silvestri, M.L.Z.; Siqueira, W.J.; de Souza, A.A.; de Souza,
A.P.; Terenzi, M.F.; Truffi, D.; Tsai, S.M.; Tsuhako, M.H.; Vallada, H.; Van
Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zago, M.A.; Zattz, M.;
Meidanis, J.; Setubal, J.C.

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF0271

Query Match 10.3%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLAL 4
|||
Db 23 SLAL 26

RESULT 34

T07290

photosystem I protein psaM - Chlorella vulgaris chloroplast

C;Species: chloroplast Chlorella vulgaris

C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000

C;Accession: T07290

R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki,
J.; Nakashima, K.; Tsudzuki, T.; Suzuki, Y.; Hamada, A.; Ohta, T.; Inamura, A.;
Yoshinaga, K.; Sugiura, M.

Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997

A;Title: Complete nucleotide sequence of the chloroplast genome from the green
alga Chlorella vulgaris: the existence of genes possibly involved in chloroplast
division.

A;Reference number: Z15985; MUID:97303241; PMID:9159184
A;Accession: T07290
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-31 <WAK>
A;Cross-references: EMBL:AB001684; NID:g2224352; PIDN:BAA57938.1; PID:g2224454
C;Genetics:
A;Gene: psaM
A;Genome: chloroplast
C;Keywords: chloroplast; membrane-associated complex; photosynthesis;
photosystem I; thylakoid

Query Match 10.3%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LALA 5
|||
Db 14 LALA 17

RESULT 35
D61014
defensin NP-1 - rat
N;Alternate names: cationic cysteine-rich peptide R-4
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: D61014; A60113
R;Belcourt, D.; Singh, A.; Bateman, A.; Lazure, C.; Solomon, S.; Bennett, H.P.J.
Regul. Pept. 40, 87-100, 1992
A;Title: Purification of cationic cystine-rich peptides from rat bone marrow.
Primary structures and biological activity of the rat corticostatin family of
peptides.
A;Reference number: A61014; MUID:93067247; PMID:1332140
A;Accession: D61014
A;Molecule type: protein
A;Residues: 1-32 <BEL>
R;Eisenhauer, P.B.; Harwig, S.L.; Szklarek, D.; Ganz, T.; Selsted, M.E.; Lehrer,
R.I.
Infect. Immun. 57, 2021-2027, 1989
A;Title: Purification and antimicrobial properties of three defensins from rat
neutrophils.
A;Reference number: A60113; MUID:89277517; PMID:2543629
A;Accession: A60113
A;Molecule type: protein
A;Residues: 1-32 <EIS>
C;Comment: Defensins are antimicrobial cationic peptides with activity against
fungi and bacteria.
C;Superfamily: mammalian defensin

Query Match 10.3%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 FRER 13
|||
Db 12 FRER 15

RESULT 36

E61014

defensin R-5 - rat

N;Alternate names: cationic cysteine-rich peptide R-5

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C;Accession: E61014

R;Belcourt, D.; Singh, A.; Bateman, A.; Lazure, C.; Solomon, S.; Bennett, H.P.J.

Regul. Pept. 40, 87-100, 1992

A;Title: Purification of cationic cystine-rich peptides from rat bone marrow.

Primary structures and biological activity of the rat corticostatin family of peptides.

A;Reference number: A61014; MUID:93067247; PMID:1332140

A;Accession: E61014

A;Molecule type: protein

A;Residues: 1-32 <BEL>

C;Comment: Defensins are antimicrobial cationic peptides with activity against fungi and bacteria.

C;Superfamily: mammalian defensin

Query Match 10.3%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 FRER 13
||||
Db 12 FRER 15

RESULT 37

A25735

interphotoreceptor retinoid-binding protein - rhesus macaque (fragment)

N;Alternate names: interstitial retinol-binding protein

C;Species: Macaca mulatta (rhesus macaque)

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 21-Nov-1997

C;Accession: A25735; E24417

R;Redmond, T.M.; Wiggert, B.; Robey, F.A.; Chader, G.J.

Biochem. J. 240, 19-26, 1986

A;Title: Interspecies conservation of structure of interphotoreceptor retinoid-binding protein. Similarities and differences as adjudged by peptide mapping and N-terminal sequencing.

A;Reference number: A90335; MUID:87156570; PMID:3827838

A;Accession: A25735

A;Molecule type: protein

A;Residues: 1-32 <RED>

R;Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.

FEBS Lett. 205, 309-312, 1986

A;Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10 vertebrate species.

A;Reference number: A91365; MUID:86301171; PMID:3743780

A;Accession: E24417

A;Molecule type: protein

A;Residues: 1-4, 'X', 6-22 <FON>

C;Superfamily: interphotoreceptor retinoid-binding protein

C;Keywords: duplication

Query Match 10.3%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 LVLD 37
|||
Db 10 LVLD 13

RESULT 38

C84355

hypothetical protein Vng2049c [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: C84355

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.; Hall, J.; Dahl, T.A.; Welti, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.; Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich, J.L.; Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: C84355

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-32 <STO>

A;Cross-references: GB:AE004437; NID:g10581474; PIDN:AAG20207.1; GSPDB:GN00138

C;Genetics:

A;Gene: VNG2049C

Query Match 10.3%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERA 14
|||
Db 15 RERA 18

RESULT 39

PC7067

meltrin beta - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 20-Jun-2000

C;Accession: PC7067

R;Kurohara, K.; Matsuda, Y.; Nagabukuro, A.; Tsuji, A.; Amagasa, T.; Fujisawa-Sehara, A.

Biochem. Biophys. Res. Commun. 270, 522-527, 2000

A;Title: Meltrin beta (ADAM19) gene: Cloning, mapping, and analysis of the regulatory region.

A;Reference number: PC7067

A;Accession: PC7067
A;Molecule type: mRNA
A;Residues: 1-32 <KUR>
C;Comment: This protein, a member of the membrane-bound metalloprotease-disintegrin family, functions in the morphogenesis.
C;Genetics:
A;Map position: 11A5-B1.1
C;Keywords: membrane bound; metalloproteinase

Query Match 10.3%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
||||
Db 13 LALA 16

RESULT 40

A44181
Cerastes serine proteinase (EC 3.4.21.-) - horn viper (fragment)
N;Alternate names: proteinase RP34
C;Species: Cerastes cerastes (horn viper)

C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 19-May-2000
C;Accession: A44181

R;Laraba-Djebari, F.; Martin-Eauclaire, M.F.; Marchot, P.
Toxicon 30, 1399-1410, 1992

A;Title: A fibrinogen-clotting serine proteinase from Cerastes cerastes (horned viper) venom with arginine-esterase and amidase activities. Purification, characterization and kinetic parameter determination.

A;Reference number: A44181; MUID:93134605; PMID:1485336

A;Accession: A44181

A;Molecule type: protein

A;Residues: 1-33 <LAR>

A;Experimental source: venom

A;Note: sequence extracted from NCBI backbone (NCBIP:122484)

C;Superfamily: trypsin; trypsin homology

C;Keywords: hydrolase; serine proteinase; venom

Query Match 10.3%; Score 4; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLAL 4
||||
Db 14 SLAL 17

Search completed: January 14, 2004, 10:37:36
Job time : 15.5421 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:37:44 ; Search time 26.243 Seconds
(without alignments)
303.882 Million cell updates/sec

Title: US-09-843-221A-170

Perfect score: 39

Sequence: 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 762491 seqs, 204481190 residues

Word size : 0

Total number of hits satisfying chosen parameters: 28045

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query
No. Score Match Length DB ID Description

1	39	100.0	39	11	US-09-843-221A-160	Sequence 160, Appl
2	39	100.0	39	11	US-09-843-221A-170	Sequence 170, Appl
3	39	100.0	39	15	US-10-014-162-1	Sequence 1, Appl
4	38	97.4	38	15	US-10-014-162-2	Sequence 2, Appl
5	38	97.4	38	15	US-10-014-162-38	Sequence 38, Appl
6	37	94.9	37	15	US-10-014-162-3	Sequence 3, Appl
7	37	94.9	37	15	US-10-014-162-39	Sequence 39, Appl
8	36	92.3	36	15	US-10-014-162-4	Sequence 4, Appl
9	36	92.3	36	15	US-10-014-162-40	Sequence 40, Appl
10	35	89.7	35	15	US-10-014-162-5	Sequence 5, Appl
11	35	89.7	35	15	US-10-014-162-41	Sequence 41, Appl
12	34	87.2	34	15	US-10-014-162-6	Sequence 6, Appl
13	34	87.2	34	15	US-10-014-162-42	Sequence 42, Appl
14	33	84.6	33	15	US-10-014-162-7	Sequence 7, Appl
15	33	84.6	33	15	US-10-014-162-43	Sequence 43, Appl
16	32	82.1	32	15	US-10-014-162-8	Sequence 8, Appl
17	32	82.1	32	15	US-10-014-162-44	Sequence 44, Appl
18	31	79.5	31	15	US-10-014-162-9	Sequence 9, Appl
19	31	79.5	31	15	US-10-014-162-45	Sequence 45, Appl
20	31	79.5	31	15	US-10-014-162-78	Sequence 78, Appl
21	30	76.9	30	15	US-10-014-162-10	Sequence 10, Appl
22	30	76.9	30	15	US-10-014-162-46	Sequence 46, Appl
23	30	76.9	30	15	US-10-014-162-79	Sequence 79, Appl
24	29	74.4	29	15	US-10-014-162-11	Sequence 11, Appl
25	29	74.4	29	15	US-10-014-162-47	Sequence 47, Appl
26	29	74.4	29	15	US-10-014-162-80	Sequence 80, Appl
27	28	71.8	28	15	US-10-014-162-48	Sequence 48, Appl
28	6	15.4	28	12	US-10-154-884B-11122	Sequence 11122, A
29	6	15.4	31	12	US-10-154-884B-11106	Sequence 11106, A
30	6	15.4	37	15	US-10-026-741-7	Sequence 7, Appl
31	6	15.4	38	9	US-09-779-451-40	Sequence 40, Appl
32	5	12.8	28	9	US-09-864-761-37845	Sequence 37845, A
33	5	12.8	28	9	US-09-864-761-38197	Sequence 38197, A
34	5	12.8	28	9	US-09-864-761-45958	Sequence 45958, A
35	5	12.8	28	9	US-09-782-980-145	Sequence 145, App
36	5	12.8	28	11	US-09-776-724A-114	Sequence 114, App
37	5	12.8	28	14	US-10-001-887-123	Sequence 123, App
38	5	12.8	29	10	US-09-905-831-12	Sequence 12, Appl
39	5	12.8	29	10	US-09-905-831-14	Sequence 14, Appl
40	5	12.8	29	10	US-09-905-831-15	Sequence 15, Appl
41	5	12.8	29	11	US-09-259-658-15	Sequence 15, Appl
42	5	12.8	29	11	US-09-820-843A-22	Sequence 22, Appl
43	5	12.8	29	11	US-09-491-614-14	Sequence 14, Appl
44	5	12.8	29	11	US-09-491-614-15	Sequence 15, Appl
45	5	12.8	29	15	US-10-103-597A-8	Sequence 8, Appl
46	5	12.8	29	15	US-10-161-205-13	Sequence 13, Appl
47	5	12.8	29	15	US-10-101-001-13	Sequence 13, Appl
48	5	12.8	29	15	US-10-188-444-8	Sequence 8, Appl
49	5	12.8	30	12	US-09-933-767-614	Sequence 614, App
50	5	12.8	30	15	US-10-023-282-614	Sequence 614, App
51	5	12.8	32	9	US-09-791-946-3	Sequence 3, Appl
52	5	12.8	32	12	US-10-164-279-11	Sequence 11, Appl
53	5	12.8	32	12	US-09-791-551-33	Sequence 33, Appl
54	5	12.8	33	9	US-09-864-761-33569	Sequence 33569, A
55	5	12.8	33	12	US-10-164-279-2	Sequence 2, Appl
56	5	12.8	35	12	US-10-153-244-319	Sequence 319, App

57	5	12.8	35	12	US-10-153-244-333	Sequence 333, App
58	5	12.8	35	12	US-10-264-049-3193	Sequence 3193, Ap
59	5	12.8	37	9	US-09-864-761-34924	Sequence 34924, A
60	5	12.8	38	10	US-09-919-473-12	Sequence 12, Appl
61	5	12.8	38	12	US-10-029-386-31288	Sequence 31288, A
62	5	12.8	38	15	US-10-099-766-6	Sequence 6, Appli
63	5	12.8	39	9	US-09-864-761-44798	Sequence 44798, A
64	5	12.8	39	12	US-10-153-244-330	Sequence 330, App
65	5	12.8	39	12	US-10-315-964A-287	Sequence 287, App
66	5	12.8	39	12	US-10-315-964A-288	Sequence 288, App
67	5	12.8	39	12	US-10-317-251A-287	Sequence 287, App
68	5	12.8	39	12	US-10-317-251A-288	Sequence 288, App
69	5	12.8	39	12	US-10-317-252A-287	Sequence 287, App
70	5	12.8	39	12	US-10-317-252A-288	Sequence 288, App
71	5	12.8	39	14	US-10-002-344A-217	Sequence 217, App
72	5	12.8	40	9	US-09-682-706-15	Sequence 15, Appl
73	5	12.8	40	12	US-10-315-964A-21	Sequence 21, Appl
74	5	12.8	40	12	US-10-315-964A-23	Sequence 23, Appl
75	5	12.8	40	12	US-10-315-964A-279	Sequence 279, App
76	5	12.8	40	12	US-10-315-964A-281	Sequence 281, App
77	5	12.8	40	12	US-10-315-964A-282	Sequence 282, App
78	5	12.8	40	12	US-10-315-964A-285	Sequence 285, App
79	5	12.8	40	12	US-10-315-964A-286	Sequence 286, App
80	5	12.8	40	12	US-10-315-964A-289	Sequence 289, App
81	5	12.8	40	12	US-10-315-964A-290	Sequence 290, App
82	5	12.8	40	12	US-10-315-964A-291	Sequence 291, App
83	5	12.8	40	12	US-10-315-964A-292	Sequence 292, App
84	5	12.8	40	12	US-10-315-964A-294	Sequence 294, App
85	5	12.8	40	12	US-10-315-964A-295	Sequence 295, App
86	5	12.8	40	12	US-10-315-964A-373	Sequence 373, App
87	5	12.8	40	12	US-10-315-964A-375	Sequence 375, App
88	5	12.8	40	12	US-10-315-964A-377	Sequence 377, App
89	5	12.8	40	12	US-10-315-964A-378	Sequence 378, App
90	5	12.8	40	12	US-10-315-964A-379	Sequence 379, App
91	5	12.8	40	12	US-10-315-964A-381	Sequence 381, App
92	5	12.8	40	12	US-10-315-964A-383	Sequence 383, App
93	5	12.8	40	12	US-10-317-251A-21	Sequence 21, Appl
94	5	12.8	40	12	US-10-317-251A-23	Sequence 23, Appl
95	5	12.8	40	12	US-10-317-251A-279	Sequence 279, App
96	5	12.8	40	12	US-10-317-251A-281	Sequence 281, App
97	5	12.8	40	12	US-10-317-251A-282	Sequence 282, App
98	5	12.8	40	12	US-10-317-251A-285	Sequence 285, App
99	5	12.8	40	12	US-10-317-251A-286	Sequence 286, App
100	5	12.8	40	12	US-10-317-251A-289	Sequence 289, App
101	5	12.8	40	12	US-10-317-251A-290	Sequence 290, App
102	5	12.8	40	12	US-10-317-251A-291	Sequence 291, App
103	5	12.8	40	12	US-10-317-251A-292	Sequence 292, App
104	5	12.8	40	12	US-10-317-251A-294	Sequence 294, App
105	5	12.8	40	12	US-10-317-251A-295	Sequence 295, App
106	5	12.8	40	12	US-10-317-251A-373	Sequence 373, App
107	5	12.8	40	12	US-10-317-251A-375	Sequence 375, App
108	5	12.8	40	12	US-10-317-251A-377	Sequence 377, App
109	5	12.8	40	12	US-10-317-251A-378	Sequence 378, App
110	5	12.8	40	12	US-10-317-251A-379	Sequence 379, App
111	5	12.8	40	12	US-10-317-251A-381	Sequence 381, App
112	5	12.8	40	12	US-10-317-251A-383	Sequence 383, App
113	5	12.8	40	12	US-10-317-252A-21	Sequence 21, Appl

114	5	12.8	40	12	US-10-317-252A-23	Sequence 23, Appl
115	5	12.8	40	12	US-10-317-252A-279	Sequence 279, App
116	5	12.8	40	12	US-10-317-252A-281	Sequence 281, App
117	5	12.8	40	12	US-10-317-252A-282	Sequence 282, App
118	5	12.8	40	12	US-10-317-252A-285	Sequence 285, App
119	5	12.8	40	12	US-10-317-252A-286	Sequence 286, App
120	5	12.8	40	12	US-10-317-252A-289	Sequence 289, App
121	5	12.8	40	12	US-10-317-252A-290	Sequence 290, App
122	5	12.8	40	12	US-10-317-252A-291	Sequence 291, App
123	5	12.8	40	12	US-10-317-252A-292	Sequence 292, App
124	5	12.8	40	12	US-10-317-252A-294	Sequence 294, App
125	5	12.8	40	12	US-10-317-252A-295	Sequence 295, App
126	5	12.8	40	12	US-10-317-252A-373	Sequence 373, App
127	5	12.8	40	12	US-10-317-252A-375	Sequence 375, App
128	5	12.8	40	12	US-10-317-252A-377	Sequence 377, App
129	5	12.8	40	12	US-10-317-252A-378	Sequence 378, App
130	5	12.8	40	12	US-10-317-252A-379	Sequence 379, App
131	5	12.8	40	12	US-10-317-252A-381	Sequence 381, App
132	5	12.8	40	12	US-10-317-252A-383	Sequence 383, App
133	5	12.8	40	14	US-10-105-992-11	Sequence 11, Appl
134	5	12.8	40	15	US-10-116-252-40	Sequence 40, Appl
135	4	10.3	28	9	US-09-864-761-33901	Sequence 33901, A
136	4	10.3	28	9	US-09-864-761-37919	Sequence 37919, A
137	4	10.3	28	9	US-09-864-761-39629	Sequence 39629, A
138	4	10.3	28	9	US-09-864-761-40300	Sequence 40300, A
139	4	10.3	28	9	US-09-864-761-41850	Sequence 41850, A
140	4	10.3	28	9	US-09-847-539A-3	Sequence 3, Appli
141	4	10.3	28	9	US-09-728-721-19	Sequence 19, Appl
142	4	10.3	28	9	US-09-782-980-146	Sequence 146, App
143	4	10.3	28	9	US-09-929-818-42	Sequence 42, Appl
144	4	10.3	28	9	US-09-929-818-138	Sequence 138, App
145	4	10.3	28	10	US-09-935-291A-21	Sequence 21, Appl
146	4	10.3	28	10	US-09-893-737-136	Sequence 136, App
147	4	10.3	28	10	US-09-896-888A-31	Sequence 31, Appl
148	4	10.3	28	11	US-09-974-879-345	Sequence 345, App
149	4	10.3	28	11	US-09-809-391-520	Sequence 520, App
150	4	10.3	28	11	US-09-305-736-345	Sequence 345, App
151	4	10.3	28	12	US-10-293-086-57	Sequence 57, Appl
152	4	10.3	28	12	US-10-303-090B-7	Sequence 7, Appli
153	4	10.3	28	12	US-09-882-171-520	Sequence 520, App
154	4	10.3	28	12	US-10-231-417-591	Sequence 591, App
155	4	10.3	28	12	US-10-314-506-17	Sequence 17, Appl
156	4	10.3	28	12	US-10-016-986-13	Sequence 13, Appl
157	4	10.3	28	12	US-10-189-437-729	Sequence 729, App
158	4	10.3	28	12	US-09-818-683-345	Sequence 345, App
159	4	10.3	28	12	US-10-283-940-40	Sequence 40, Appl
160	4	10.3	28	12	US-10-366-125-23	Sequence 23, Appl
161	4	10.3	28	14	US-10-012-452-7	Sequence 7, Appli
162	4	10.3	28	14	US-10-014-269-17	Sequence 17, Appl
163	4	10.3	28	14	US-10-105-931-19	Sequence 19, Appl
164	4	10.3	28	14	US-10-002-974-17	Sequence 17, Appl
165	4	10.3	28	14	US-10-118-984-19	Sequence 19, Appl
166	4	10.3	28	15	US-10-097-065-389	Sequence 389, App
167	4	10.3	28	15	US-10-144-929-241	Sequence 241, App
168	4	10.3	28	15	US-10-295-981-19	Sequence 19, Appl
169	4	10.3	28	15	US-10-272-339A-30	Sequence 30, Appl
170	4	10.3	28	15	US-10-081-872-222	Sequence 222, App

171	4	10.3	29	9	US-09-835-147-12	Sequence 12, Appl
172	4	10.3	29	9	US-09-904-380-26	Sequence 26, Appl
173	4	10.3	29	9	US-09-904-380-27	Sequence 27, Appl
174	4	10.3	29	9	US-09-932-161-1	Sequence 1, Appli
175	4	10.3	29	9	US-09-864-761-38832	Sequence 38832, A
176	4	10.3	29	9	US-09-864-761-39320	Sequence 39320, A
177	4	10.3	29	9	US-09-864-761-40009	Sequence 40009, A
178	4	10.3	29	9	US-09-864-761-44425	Sequence 44425, A
179	4	10.3	29	9	US-09-864-761-45207	Sequence 45207, A
180	4	10.3	29	9	US-09-864-761-47197	Sequence 47197, A
181	4	10.3	29	10	US-09-935-291A-36	Sequence 36, Appl
182	4	10.3	29	11	US-09-809-391-743	Sequence 743, App
183	4	10.3	29	11	US-09-969-730-196	Sequence 196, App
184	4	10.3	29	12	US-10-153-604A-72	Sequence 72, Appl
185	4	10.3	29	12	US-10-411-224-139	Sequence 139, App
186	4	10.3	29	12	US-10-096-777-1	Sequence 1, Appli
187	4	10.3	29	12	US-09-882-171-743	Sequence 743, App
188	4	10.3	29	12	US-10-105-232-345	Sequence 345, App
189	4	10.3	29	12	US-09-962-756-1352	Sequence 1352, Ap
190	4	10.3	29	12	US-09-962-756-1364	Sequence 1364, Ap
191	4	10.3	29	12	US-09-962-756-1365	Sequence 1365, Ap
192	4	10.3	29	12	US-09-962-756-1378	Sequence 1378, Ap
193	4	10.3	29	12	US-09-962-756-1393	Sequence 1393, Ap
194	4	10.3	29	12	US-09-962-756-1432	Sequence 1432, Ap
195	4	10.3	29	12	US-10-029-386-27864	Sequence 27864, A
196	4	10.3	29	12	US-10-029-386-29985	Sequence 29985, A
197	4	10.3	29	12	US-10-189-437-332	Sequence 332, App
198	4	10.3	29	12	US-10-364-276-4	Sequence 4, Appli
199	4	10.3	29	12	US-10-391-634-13	Sequence 13, Appl
200	4	10.3	29	12	US-10-253-471-1352	Sequence 1352, Ap
201	4	10.3	29	12	US-10-253-471-1364	Sequence 1364, Ap
202	4	10.3	29	12	US-10-253-471-1365	Sequence 1365, Ap
203	4	10.3	29	12	US-10-253-471-1378	Sequence 1378, Ap
204	4	10.3	29	12	US-10-253-471-1393	Sequence 1393, Ap
205	4	10.3	29	12	US-10-253-471-1432	Sequence 1432, Ap
206	4	10.3	29	12	US-10-047-021-139	Sequence 139, App
207	4	10.3	29	12	US-10-154-884B-11099	Sequence 11099, A
208	4	10.3	29	14	US-10-153-064-72	Sequence 72, Appl
209	4	10.3	29	14	US-10-004-381-29	Sequence 29, Appl
210	4	10.3	29	15	US-10-092-750-45	Sequence 45, Appl
211	4	10.3	29	15	US-10-092-750-58	Sequence 58, Appl
212	4	10.3	29	15	US-10-012-542-368	Sequence 368, App
213	4	10.3	29	15	US-10-026-741-33	Sequence 33, Appl
214	4	10.3	29	15	US-10-103-597A-9	Sequence 9, Appli
215	4	10.3	29	15	US-10-188-444-9	Sequence 9, Appli
216	4	10.3	29	15	US-10-106-698-7646	Sequence 7646, Ap
217	4	10.3	29	15	US-10-272-339A-46	Sequence 46, Appl
218	4	10.3	29	16	US-10-176-306-35	Sequence 35, Appl
219	4	10.3	30	8	US-08-450-842-40	Sequence 40, Appl
220	4	10.3	30	8	US-08-450-842-43	Sequence 43, Appl
221	4	10.3	30	9	US-09-864-761-38865	Sequence 38865, A
222	4	10.3	30	9	US-09-864-761-45317	Sequence 45317, A
223	4	10.3	30	10	US-09-953-510-30	Sequence 30, Appl
224	4	10.3	30	11	US-09-774-639-160	Sequence 160, App
225	4	10.3	30	11	US-09-809-391-443	Sequence 443, App
226	4	10.3	30	11	US-09-820-053A-163	Sequence 163, App
227	4	10.3	30	12	US-10-147-255-30	Sequence 30, Appl

228	4	10.3	30	12	US-10-160-162-314	Sequence 314, App
229	4	10.3	30	12	US-10-058-053A-330	Sequence 330, App
230	4	10.3	30	12	US-09-882-171-443	Sequence 443, App
231	4	10.3	30	12	US-10-071-174-21	Sequence 21, Appl
232	4	10.3	30	12	US-10-192-832-58	Sequence 58, Appl
233	4	10.3	30	12	US-10-192-832-59	Sequence 59, Appl
234	4	10.3	30	12	US-10-029-386-28555	Sequence 28555, A
235	4	10.3	30	12	US-09-820-649-314	Sequence 314, App
236	4	10.3	30	12	US-10-364-276-9	Sequence 9, Appli
237	4	10.3	30	12	US-10-057-475B-10820	Sequence 10820, A
238	4	10.3	30	12	US-10-057-475B-10821	Sequence 10821, A
239	4	10.3	30	12	US-10-057-475B-10825	Sequence 10825, A
240	4	10.3	30	12	US-10-057-475B-10826	Sequence 10826, A
241	4	10.3	30	12	US-10-057-475B-10832	Sequence 10832, A
242	4	10.3	30	12	US-10-057-475B-10833	Sequence 10833, A
243	4	10.3	30	12	US-10-154-884B-10820	Sequence 10820, A
244	4	10.3	30	12	US-10-154-884B-10821	Sequence 10821, A
245	4	10.3	30	12	US-10-154-884B-10825	Sequence 10825, A
246	4	10.3	30	12	US-10-154-884B-10826	Sequence 10826, A
247	4	10.3	30	12	US-10-154-884B-10832	Sequence 10832, A
248	4	10.3	30	12	US-10-154-884B-10833	Sequence 10833, A
249	4	10.3	30	12	US-10-154-884B-11124	Sequence 11124, A
250	4	10.3	30	12	US-10-264-049-2585	Sequence 2585, Ap
251	4	10.3	30	15	US-10-109-171-163	Sequence 163, App
252	4	10.3	30	15	US-10-081-872-228	Sequence 228, App
253	4	10.3	31	9	US-09-835-147-13	Sequence 13, Appl
254	4	10.3	31	9	US-09-864-761-35006	Sequence 35006, A
255	4	10.3	31	9	US-09-864-761-36617	Sequence 36617, A
256	4	10.3	31	9	US-09-864-761-38920	Sequence 38920, A
257	4	10.3	31	9	US-09-864-761-43498	Sequence 43498, A
258	4	10.3	31	9	US-09-864-761-44182	Sequence 44182, A
259	4	10.3	31	9	US-09-782-980-139	Sequence 139, App
260	4	10.3	31	9	US-09-142-755-10	Sequence 10, Appl
261	4	10.3	31	10	US-09-956-206A-5	Sequence 5, Appli
262	4	10.3	31	11	US-09-983-802-398	Sequence 398, App
263	4	10.3	31	11	US-09-996-069-4	Sequence 4, Appli
264	4	10.3	31	11	US-09-776-724A-183	Sequence 183, App
265	4	10.3	31	11	US-09-969-730-145	Sequence 145, App
266	4	10.3	31	11	US-09-820-053A-63	Sequence 63, App
267	4	10.3	31	12	US-10-195-730-211	Sequence 211, App
268	4	10.3	31	12	US-09-840-085-69	Sequence 69, Appl
269	4	10.3	31	12	US-09-840-085-70	Sequence 70, Appl
270	4	10.3	31	12	US-09-840-085-71	Sequence 71, Appl
271	4	10.3	31	12	US-09-840-085-72	Sequence 72, Appl
272	4	10.3	31	12	US-10-170-812-3	Sequence 3, Appli
273	4	10.3	31	12	US-10-107-857-43	Sequence 43, Appl
274	4	10.3	31	12	US-09-933-767-383	Sequence 383, App
275	4	10.3	31	12	US-10-029-386-27465	Sequence 27465, A
276	4	10.3	31	12	US-10-029-386-27619	Sequence 27619, A
277	4	10.3	31	12	US-10-366-493-74	Sequence 74, Appl
278	4	10.3	31	12	US-10-425-328-6	Sequence 6, Appli
279	4	10.3	31	12	US-10-154-884B-11108	Sequence 11108, A
280	4	10.3	31	12	US-10-154-884B-11116	Sequence 11116, A
281	4	10.3	31	12	US-10-264-049-2577	Sequence 2577, Ap
282	4	10.3	31	12	US-10-430-752A-21	Sequence 21, Appl
283	4	10.3	31	14	US-10-001-887-136	Sequence 136, App
284	4	10.3	31	15	US-10-097-065-371	Sequence 371, App

285	4	10.3	31	15	US-10-191-879-25	Sequence 25, Appl
286	4	10.3	31	15	US-10-023-282-383	Sequence 383, App
287	4	10.3	31	15	US-10-075-869-74	Sequence 74, Appl
288	4	10.3	31	15	US-10-109-171-63	Sequence 63, Appl
289	4	10.3	31	15	US-10-106-698-8191	Sequence 8191, Ap
290	4	10.3	31	15	US-10-272-339A-48	Sequence 48, Appl
291	4	10.3	32	9	US-09-030-619-193	Sequence 193, App
292	4	10.3	32	9	US-09-030-619-194	Sequence 194, App
293	4	10.3	32	9	US-09-864-761-33714	Sequence 33714, A
294	4	10.3	32	9	US-09-864-761-36183	Sequence 36183, A
295	4	10.3	32	9	US-09-917-340-48	Sequence 48, Appl
296	4	10.3	32	9	US-09-917-340-81	Sequence 81, Appl
297	4	10.3	32	11	US-09-774-639-173	Sequence 173, App
298	4	10.3	32	11	US-09-983-802-181	Sequence 181, App
299	4	10.3	32	11	US-09-847-102A-114	Sequence 114, App
300	4	10.3	32	11	US-09-847-102A-122	Sequence 122, App
301	4	10.3	32	11	US-09-847-102A-123	Sequence 123, App
302	4	10.3	32	11	US-09-563-222-124	Sequence 124, App
303	4	10.3	32	11	US-09-776-191-60	Sequence 60, Appl
304	4	10.3	32	12	US-10-262-525-25	Sequence 25, Appl
305	4	10.3	32	12	US-10-262-525-27	Sequence 27, Appl
306	4	10.3	32	12	US-10-364-360-30	Sequence 30, Appl
307	4	10.3	32	12	US-10-364-360-31	Sequence 31, Appl
308	4	10.3	32	12	US-10-029-386-34142	Sequence 34142, A
309	4	10.3	32	12	US-10-277-233-193	Sequence 193, App
310	4	10.3	32	12	US-10-277-233-194	Sequence 194, App
311	4	10.3	32	14	US-10-061-395-48	Sequence 48, Appl
312	4	10.3	32	15	US-10-083-815-66	Sequence 66, Appl
313	4	10.3	32	15	US-10-174-410-169	Sequence 169, App
314	4	10.3	32	15	US-10-174-410-225	Sequence 225, App
315	4	10.3	32	15	US-10-174-410-238	Sequence 238, App
316	4	10.3	32	15	US-10-174-410-263	Sequence 263, App
317	4	10.3	32	15	US-10-052-942-54	Sequence 54, Appl
318	4	10.3	33	9	US-09-729-835-69	Sequence 69, Appl
319	4	10.3	33	9	US-09-030-619-186	Sequence 186, App
320	4	10.3	33	9	US-09-030-619-192	Sequence 192, App
321	4	10.3	33	9	US-09-864-761-35258	Sequence 35258, A
322	4	10.3	33	9	US-09-864-761-37273	Sequence 37273, A
323	4	10.3	33	9	US-09-864-761-39198	Sequence 39198, A
324	4	10.3	33	9	US-09-864-761-46897	Sequence 46897, A
325	4	10.3	33	9	US-09-864-761-47628	Sequence 47628, A
326	4	10.3	33	9	US-09-864-761-47730	Sequence 47730, A
327	4	10.3	33	9	US-09-864-761-49033	Sequence 49033, A
328	4	10.3	33	9	US-09-975-901-17	Sequence 17, Appl
329	4	10.3	33	9	US-09-917-340-43	Sequence 43, Appl
330	4	10.3	33	9	US-09-920-975-25	Sequence 25, Appl
331	4	10.3	33	9	US-09-920-975-26	Sequence 26, Appl
332	4	10.3	33	9	US-09-920-975-27	Sequence 27, Appl
333	4	10.3	33	9	US-09-920-975-28	Sequence 28, Appl
334	4	10.3	33	9	US-09-920-975-29	Sequence 29, Appl
335	4	10.3	33	9	US-09-920-975-30	Sequence 30, Appl
336	4	10.3	33	9	US-09-920-975-31	Sequence 31, Appl
337	4	10.3	33	9	US-09-920-975-32	Sequence 32, Appl
338	4	10.3	33	9	US-09-920-975-33	Sequence 33, Appl
339	4	10.3	33	9	US-09-920-975-34	Sequence 34, Appl
340	4	10.3	33	9	US-09-920-975-35	Sequence 35, Appl
341	4	10.3	33	9	US-09-920-975-36	Sequence 36, Appl

342	4	10.3	33	9	US-09-920-975-37	Sequence 37, Appl
343	4	10.3	33	9	US-09-920-975-38	Sequence 38, Appl
344	4	10.3	33	9	US-09-920-975-39	Sequence 39, Appl
345	4	10.3	33	9	US-09-920-975-40	Sequence 40, Appl
346	4	10.3	33	9	US-09-920-975-41	Sequence 41, Appl
347	4	10.3	33	9	US-09-920-975-42	Sequence 42, Appl
348	4	10.3	33	9	US-09-920-975-43	Sequence 43, Appl
349	4	10.3	33	9	US-09-920-975-44	Sequence 44, Appl
350	4	10.3	33	9	US-09-920-975-45	Sequence 45, Appl
351	4	10.3	33	9	US-09-920-975-46	Sequence 46, Appl
352	4	10.3	33	9	US-09-920-975-47	Sequence 47, Appl
353	4	10.3	33	9	US-09-920-975-48	Sequence 48, Appl
354	4	10.3	33	9	US-09-837-867A-36	Sequence 36, Appl
355	4	10.3	33	10	US-09-840-704-16	Sequence 16, Appl
356	4	10.3	33	10	US-09-764-877-1068	Sequence 1068, Ap
357	4	10.3	33	10	US-09-925-300-1226	Sequence 1226, Ap
358	4	10.3	33	10	US-09-925-300-1514	Sequence 1514, Ap
359	4	10.3	33	11	US-09-962-969-36	Sequence 36, Appl
360	4	10.3	33	11	US-09-913-238-70	Sequence 70, Appl
361	4	10.3	33	12	US-10-195-730-228	Sequence 228, App
362	4	10.3	33	12	US-10-029-386-33476	Sequence 33476, A
363	4	10.3	33	12	US-10-277-233-186	Sequence 186, App
364	4	10.3	33	12	US-10-277-233-192	Sequence 192, App
365	4	10.3	33	15	US-10-083-815-67	Sequence 67, Appl
366	4	10.3	33	15	US-10-081-816-109	Sequence 109, App
367	4	10.3	33	15	US-10-007-280A-176	Sequence 176, App
368	4	10.3	34	9	US-09-864-761-34925	Sequence 34925, A
369	4	10.3	34	9	US-09-864-761-36948	Sequence 36948, A
370	4	10.3	34	9	US-09-864-761-41645	Sequence 41645, A
371	4	10.3	34	9	US-09-864-761-42152	Sequence 42152, A
372	4	10.3	34	9	US-09-864-761-43916	Sequence 43916, A
373	4	10.3	34	9	US-09-281-717-15	Sequence 15, Appl
374	4	10.3	34	9	US-09-281-717-18	Sequence 18, Appl
375	4	10.3	34	9	US-09-281-717-21	Sequence 21, Appl
376	4	10.3	34	9	US-09-730-989-6	Sequence 6, Appli
377	4	10.3	34	12	US-10-032-214-315	Sequence 315, App
378	4	10.3	34	12	US-10-097-111-528	Sequence 528, App
379	4	10.3	34	12	US-10-219-700-67	Sequence 67, Appl
380	4	10.3	34	12	US-10-160-162-121	Sequence 121, App
381	4	10.3	34	12	US-10-029-386-32410	Sequence 32410, A
382	4	10.3	34	12	US-09-820-649-121	Sequence 121, App
383	4	10.3	34	12	US-10-047-021-66	Sequence 66, Appl
384	4	10.3	34	14	US-10-090-378-29	Sequence 29, Appl
385	4	10.3	34	14	US-10-013-939-13	Sequence 13, Appl
386	4	10.3	34	14	US-10-013-939-17	Sequence 17, Appl
387	4	10.3	34	15	US-10-083-815-29	Sequence 29, Appl
388	4	10.3	34	15	US-10-050-882-97	Sequence 97, Appl
389	4	10.3	35	9	US-09-864-761-33364	Sequence 33364, A
390	4	10.3	35	9	US-09-864-761-35139	Sequence 35139, A
391	4	10.3	35	9	US-09-864-761-36017	Sequence 36017, A
392	4	10.3	35	9	US-09-864-761-46372	Sequence 46372, A
393	4	10.3	35	9	US-09-764-869-771	Sequence 771, App
394	4	10.3	35	9	US-09-820-893-122	Sequence 122, App
395	4	10.3	35	9	US-09-779-451-39	Sequence 39, Appl
396	4	10.3	35	12	US-09-930-915A-4	Sequence 4, Appli
397	4	10.3	35	12	US-10-219-700-46	Sequence 46, Appl
398	4	10.3	35	12	US-10-411-224-66	Sequence 66, Appl

399	4	10.3	35	12	US-10-340-484-13	Sequence 13, Appl
400	4	10.3	35	12	US-10-074-511-91	Sequence 91, Appl
401	4	10.3	35	12	US-10-341-200-16	Sequence 16, Appl
402	4	10.3	35	12	US-10-289-135A-33	Sequence 33, Appl
403	4	10.3	35	12	US-10-289-135A-127	Sequence 127, App
404	4	10.3	35	12	US-10-082-014-10	Sequence 10, Appl
405	4	10.3	35	12	US-10-351-641-458	Sequence 458, App
406	4	10.3	35	12	US-10-351-641-459	Sequence 459, App
407	4	10.3	35	12	US-10-351-641-460	Sequence 460, App
408	4	10.3	35	12	US-10-351-641-461	Sequence 461, App
409	4	10.3	35	12	US-10-351-641-462	Sequence 462, App
410	4	10.3	35	12	US-10-351-641-463	Sequence 463, App
411	4	10.3	35	12	US-10-351-641-464	Sequence 464, App
412	4	10.3	35	12	US-10-351-641-465	Sequence 465, App
413	4	10.3	35	12	US-10-351-641-466	Sequence 466, App
414	4	10.3	35	12	US-10-351-641-467	Sequence 467, App
415	4	10.3	35	12	US-10-351-641-468	Sequence 468, App
416	4	10.3	35	12	US-10-351-641-469	Sequence 469, App
417	4	10.3	35	12	US-10-351-641-470	Sequence 470, App
418	4	10.3	35	12	US-10-351-641-471	Sequence 471, App
419	4	10.3	35	12	US-10-351-641-472	Sequence 472, App
420	4	10.3	35	12	US-10-351-641-473	Sequence 473, App
421	4	10.3	35	12	US-10-351-641-474	Sequence 474, App
422	4	10.3	35	12	US-10-351-641-475	Sequence 475, App
423	4	10.3	35	12	US-10-351-641-476	Sequence 476, App
424	4	10.3	35	12	US-10-351-641-477	Sequence 477, App
425	4	10.3	35	12	US-10-351-641-478	Sequence 478, App
426	4	10.3	35	12	US-10-351-641-479	Sequence 479, App
427	4	10.3	35	12	US-10-351-641-480	Sequence 480, App
428	4	10.3	35	12	US-10-351-641-481	Sequence 481, App
429	4	10.3	35	12	US-10-351-641-482	Sequence 482, App
430	4	10.3	35	12	US-10-351-641-483	Sequence 483, App
431	4	10.3	35	12	US-10-351-641-518	Sequence 518, App
432	4	10.3	35	12	US-10-351-641-519	Sequence 519, App
433	4	10.3	35	12	US-10-351-641-717	Sequence 717, App
434	4	10.3	35	12	US-10-351-641-1220	Sequence 1220, Ap
435	4	10.3	35	12	US-10-351-641-1221	Sequence 1221, Ap
436	4	10.3	35	12	US-10-351-641-1222	Sequence 1222, Ap
437	4	10.3	35	12	US-10-029-386-29768	Sequence 29768, A
438	4	10.3	35	12	US-10-029-386-30594	Sequence 30594, A
439	4	10.3	35	12	US-10-372-076-10	Sequence 10, Appl
440	4	10.3	35	12	US-10-220-587-18	Sequence 18, Appl
441	4	10.3	35	12	US-10-227-577-771	Sequence 771, App
442	4	10.3	35	14	US-10-029-217A-17	Sequence 17, Appl
443	4	10.3	35	14	US-10-029-217A-18	Sequence 18, Appl
444	4	10.3	35	15	US-10-000-256A-234	Sequence 234, App
445	4	10.3	35	15	US-10-026-741-101	Sequence 101, App
446	4	10.3	35	15	US-10-045-465-13	Sequence 13, Appl
447	4	10.3	35	15	US-10-004-530A-10	Sequence 10, Appl
448	4	10.3	35	15	US-10-050-704-193	Sequence 193, App
449	4	10.3	35	15	US-10-091-504-771	Sequence 771, App
450	4	10.3	35	15	US-10-043-344-53	Sequence 53, Appl
451	4	10.3	35	15	US-10-161-205-34	Sequence 34, Appl
452	4	10.3	35	15	US-10-101-001-34	Sequence 34, Appl
453	4	10.3	35	15	US-10-106-698-4684	Sequence 4684, Ap
454	4	10.3	35	15	US-10-106-698-8553	Sequence 8553, Ap
455	4	10.3	35	15	US-10-176-884-83	Sequence 83, Appl

456	4	10.3	35	16	US-10-318-200-33	Sequence 33, Appl
457	4	10.3	36	9	US-09-726-643-163	Sequence 163, App
458	4	10.3	36	9	US-09-864-761-38938	Sequence 38938, A
459	4	10.3	36	9	US-09-864-761-39411	Sequence 39411, A
460	4	10.3	36	9	US-09-864-761-41216	Sequence 41216, A
461	4	10.3	36	9	US-09-864-761-44493	Sequence 44493, A
462	4	10.3	36	9	US-09-864-761-46707	Sequence 46707, A
463	4	10.3	36	9	US-09-864-761-48628	Sequence 48628, A
464	4	10.3	36	9	US-09-764-869-670	Sequence 670, App
465	4	10.3	36	9	US-09-764-898-231	Sequence 231, App
466	4	10.3	36	12	US-10-123-101-59	Sequence 59, Appl
467	4	10.3	36	12	US-10-123-101-60	Sequence 60, Appl
468	4	10.3	36	12	US-10-072-301-8	Sequence 8, Appli
469	4	10.3	36	12	US-10-316-253-127	Sequence 127, App
470	4	10.3	36	12	US-10-316-253-147	Sequence 147, App
471	4	10.3	36	12	US-10-071-866-8	Sequence 8, Appli
472	4	10.3	36	12	US-10-289-135A-32	Sequence 32, Appl
473	4	10.3	36	12	US-10-351-641-541	Sequence 541, App
474	4	10.3	36	12	US-10-351-641-542	Sequence 542, App
475	4	10.3	36	12	US-10-351-641-751	Sequence 751, App
476	4	10.3	36	12	US-10-351-641-1034	Sequence 1034, Ap
477	4	10.3	36	12	US-10-351-641-1705	Sequence 1705, Ap
478	4	10.3	36	12	US-09-962-756-1315	Sequence 1315, Ap
479	4	10.3	36	12	US-09-962-756-1323	Sequence 1323, Ap
480	4	10.3	36	12	US-10-029-386-27625	Sequence 27625, A
481	4	10.3	36	12	US-10-029-386-27801	Sequence 27801, A
482	4	10.3	36	12	US-10-029-386-32339	Sequence 32339, A
483	4	10.3	36	12	US-10-029-386-33232	Sequence 33232, A
484	4	10.3	36	12	US-10-029-386-33240	Sequence 33240, A
485	4	10.3	36	12	US-10-360-828-8	Sequence 8, Appli
486	4	10.3	36	12	US-10-310-734-89	Sequence 89, Appl
487	4	10.3	36	12	US-10-310-734-90	Sequence 90, Appl
488	4	10.3	36	12	US-10-253-471-1315	Sequence 1315, Ap
489	4	10.3	36	12	US-10-253-471-1323	Sequence 1323, Ap
490	4	10.3	36	12	US-10-227-577-670	Sequence 670, App
491	4	10.3	36	12	US-10-264-049-2232	Sequence 2232, Ap
492	4	10.3	36	12	US-10-264-049-3653	Sequence 3653, Ap
493	4	10.3	36	14	US-10-001-843-139	Sequence 139, App
494	4	10.3	36	14	US-10-042-141-163	Sequence 163, App
495	4	10.3	36	15	US-10-045-465-9	Sequence 9, Appli
496	4	10.3	36	15	US-10-050-704-198	Sequence 198, App
497	4	10.3	36	15	US-10-091-504-670	Sequence 670, App
498	4	10.3	36	15	US-10-106-698-4780	Sequence 4780, Ap
499	4	10.3	37	9	US-09-205-658-100	Sequence 100, App
500	4	10.3	37	9	US-09-864-761-35194	Sequence 35194, A
501	4	10.3	37	9	US-09-864-761-35261	Sequence 35261, A
502	4	10.3	37	9	US-09-864-761-39120	Sequence 39120, A
503	4	10.3	37	9	US-09-864-761-42773	Sequence 42773, A
504	4	10.3	37	9	US-09-864-761-44628	Sequence 44628, A
505	4	10.3	37	9	US-09-864-761-45971	Sequence 45971, A
506	4	10.3	37	9	US-09-764-869-661	Sequence 661, App
507	4	10.3	37	10	US-09-770-102A-33	Sequence 33, Appl
508	4	10.3	37	11	US-09-986-480-313	Sequence 313, App
509	4	10.3	37	11	US-09-892-877-366	Sequence 366, App
510	4	10.3	37	11	US-09-948-783-370	Sequence 370, App
511	4	10.3	37	12	US-10-097-111-511	Sequence 511, App
512	4	10.3	37	12	US-10-195-730-234	Sequence 234, App

513	4	10.3	37	12	US-10-195-730-244	Sequence 244, App
514	4	10.3	37	12	US-10-315-515-80	Sequence 80, Appl
515	4	10.3	37	12	US-10-231-417-537	Sequence 537, App
516	4	10.3	37	12	US-09-963-693-100	Sequence 100, App
517	4	10.3	37	12	US-10-029-386-32797	Sequence 32797, A
518	4	10.3	37	12	US-10-357-884-7	Sequence 7, Appl
519	4	10.3	37	12	US-10-227-577-661	Sequence 661, App
520	4	10.3	37	14	US-10-001-857-127	Sequence 127, App
521	4	10.3	37	15	US-10-012-542-265	Sequence 265, App
522	4	10.3	37	15	US-10-026-741-84	Sequence 84, Appl
523	4	10.3	37	15	US-10-026-741-86	Sequence 86, Appl
524	4	10.3	37	15	US-10-026-741-90	Sequence 90, Appl
525	4	10.3	37	15	US-10-026-741-94	Sequence 94, Appl
526	4	10.3	37	15	US-10-091-504-661	Sequence 661, App
527	4	10.3	37	15	US-10-106-698-6430	Sequence 6430, Ap
528	4	10.3	37	15	US-10-156-761-12455	Sequence 12455, A
529	4	10.3	38	9	US-09-864-761-34759	Sequence 34759, A
530	4	10.3	38	9	US-09-864-761-36997	Sequence 36997, A
531	4	10.3	38	9	US-09-864-761-37421	Sequence 37421, A
532	4	10.3	38	9	US-09-864-761-39173	Sequence 39173, A
533	4	10.3	38	9	US-09-864-761-41137	Sequence 41137, A
534	4	10.3	38	9	US-09-864-761-46003	Sequence 46003, A
535	4	10.3	38	9	US-09-864-761-46302	Sequence 46302, A
536	4	10.3	38	9	US-09-779-451-12	Sequence 12, Appl
537	4	10.3	38	9	US-09-779-451-18	Sequence 18, Appl
538	4	10.3	38	9	US-09-779-451-28	Sequence 28, Appl
539	4	10.3	38	10	US-09-925-442-36	Sequence 36, Appl
540	4	10.3	38	10	US-09-908-153B-48	Sequence 48, Appl
541	4	10.3	38	10	US-09-908-153B-51	Sequence 51, Appl
542	4	10.3	38	11	US-09-986-480-417	Sequence 417, App
543	4	10.3	38	11	US-09-820-843A-105	Sequence 105, App
544	4	10.3	38	11	US-09-892-877-342	Sequence 342, App
545	4	10.3	38	11	US-09-948-783-282	Sequence 282, App
546	4	10.3	38	12	US-10-315-964A-119	Sequence 119, App
547	4	10.3	38	12	US-10-315-964A-160	Sequence 160, App
548	4	10.3	38	12	US-10-315-964A-331	Sequence 331, App
549	4	10.3	38	12	US-10-315-964A-332	Sequence 332, App
550	4	10.3	38	12	US-10-315-964A-333	Sequence 333, App
551	4	10.3	38	12	US-10-315-964A-344	Sequence 344, App
552	4	10.3	38	12	US-10-315-964A-348	Sequence 348, App
553	4	10.3	38	12	US-10-317-251A-119	Sequence 119, App
554	4	10.3	38	12	US-10-317-251A-160	Sequence 160, App
555	4	10.3	38	12	US-10-317-251A-331	Sequence 331, App
556	4	10.3	38	12	US-10-317-251A-332	Sequence 332, App
557	4	10.3	38	12	US-10-317-251A-333	Sequence 333, App
558	4	10.3	38	12	US-10-317-251A-344	Sequence 344, App
559	4	10.3	38	12	US-10-317-251A-348	Sequence 348, App
560	4	10.3	38	12	US-10-317-252A-119	Sequence 119, App
561	4	10.3	38	12	US-10-317-252A-160	Sequence 160, App
562	4	10.3	38	12	US-10-317-252A-331	Sequence 331, App
563	4	10.3	38	12	US-10-317-252A-332	Sequence 332, App
564	4	10.3	38	12	US-10-317-252A-333	Sequence 333, App
565	4	10.3	38	12	US-10-317-252A-344	Sequence 344, App
566	4	10.3	38	12	US-10-317-252A-348	Sequence 348, App
567	4	10.3	38	12	US-10-339-740-227	Sequence 227, App
568	4	10.3	38	12	US-10-351-641-83	Sequence 83, Appl
569	4	10.3	38	14	US-10-001-870-197	Sequence 197, App

570	4	10.3	38	14	US-10-004-381-35	Sequence 35, Appl
571	4	10.3	38	14	US-10-001-876-207	Sequence 207, App
572	4	10.3	38	15	US-10-034-934-97	Sequence 97, Appl
573	4	10.3	38	15	US-10-300-616-34	Sequence 34, Appl
574	4	10.3	38	15	US-10-106-698-4430	Sequence 4430, Ap
575	4	10.3	38	15	US-10-106-698-7133	Sequence 7133, Ap
576	4	10.3	38	15	US-10-106-698-8121	Sequence 8121, Ap
577	4	10.3	39	9	US-09-739-907-192	Sequence 192, App
578	4	10.3	39	9	US-09-220-920-48	Sequence 48, Appl
579	4	10.3	39	9	US-09-843-845-12	Sequence 12, Appl
580	4	10.3	39	9	US-09-946-239-13	Sequence 13, Appl
581	4	10.3	39	9	US-09-864-761-35216	Sequence 35216, A
582	4	10.3	39	9	US-09-864-761-40328	Sequence 40328, A
583	4	10.3	39	9	US-09-864-761-41084	Sequence 41084, A
584	4	10.3	39	9	US-09-864-761-44780	Sequence 44780, A
585	4	10.3	39	9	US-09-814-122-84	Sequence 84, Appl
586	4	10.3	39	9	US-09-764-869-1050	Sequence 1050, Ap
587	4	10.3	39	10	US-09-910-071-2	Sequence 2, Appl
588	4	10.3	39	10	US-09-925-300-1579	Sequence 1579, Ap
589	4	10.3	39	10	US-09-984-245-123	Sequence 123, App
590	4	10.3	39	11	US-09-983-802-384	Sequence 384, App
591	4	10.3	39	11	US-09-983-802-672	Sequence 672, App
592	4	10.3	39	11	US-09-991-209-47	Sequence 47, Appl
593	4	10.3	39	11	US-09-966-262-123	Sequence 123, App
594	4	10.3	39	11	US-09-983-966-123	Sequence 123, App
595	4	10.3	39	12	US-10-219-700-66	Sequence 66, Appl
596	4	10.3	39	12	US-10-289-660-161	Sequence 161, App
597	4	10.3	39	12	US-10-061-607A-57	Sequence 57, Appl
598	4	10.3	39	12	US-09-933-767-354	Sequence 354, App
599	4	10.3	39	12	US-09-933-767-559	Sequence 559, App
600	4	10.3	39	12	US-09-933-767-1206	Sequence 1206, Ap
601	4	10.3	39	12	US-10-351-641-1457	Sequence 1457, Ap
602	4	10.3	39	12	US-10-351-641-1529	Sequence 1529, Ap
603	4	10.3	39	12	US-09-962-756-177	Sequence 177, App
604	4	10.3	39	12	US-09-962-756-182	Sequence 182, App
605	4	10.3	39	12	US-09-962-756-203	Sequence 203, App
606	4	10.3	39	12	US-09-962-756-209	Sequence 209, App
607	4	10.3	39	12	US-09-962-756-241	Sequence 241, App
608	4	10.3	39	12	US-10-029-386-30925	Sequence 30925, A
609	4	10.3	39	12	US-10-029-386-31147	Sequence 31147, A
610	4	10.3	39	12	US-10-029-386-33749	Sequence 33749, A
611	4	10.3	39	12	US-10-060-634C-8	Sequence 8, Appl
612	4	10.3	39	12	US-10-253-471-177	Sequence 177, App
613	4	10.3	39	12	US-10-253-471-182	Sequence 182, App
614	4	10.3	39	12	US-10-253-471-203	Sequence 203, App
615	4	10.3	39	12	US-10-253-471-209	Sequence 209, App
616	4	10.3	39	12	US-10-253-471-241	Sequence 241, App
617	4	10.3	39	12	US-09-938-671-192	Sequence 192, App
618	4	10.3	39	12	US-10-227-577-1050	Sequence 1050, Ap
619	4	10.3	39	14	US-10-004-381-27	Sequence 27, Appl
620	4	10.3	39	15	US-10-091-504-1050	Sequence 1050, Ap
621	4	10.3	39	15	US-10-143-090-123	Sequence 123, App
622	4	10.3	39	15	US-10-133-128-161	Sequence 161, App
623	4	10.3	39	15	US-10-023-282-354	Sequence 354, App
624	4	10.3	39	15	US-10-023-282-559	Sequence 559, App
625	4	10.3	39	15	US-10-023-282-1206	Sequence 1206, Ap
626	4	10.3	39	15	US-10-050-882-125	Sequence 125, App

627	4	10.3	39	15	US-10-106-698-4999	Sequence 4999, Ap
628	4	10.3	39	15	US-10-106-698-6426	Sequence 6426, Ap
629	4	10.3	39	15	US-10-106-698-7613	Sequence 7613, Ap
630	4	10.3	39	16	US-10-061-043A-8	Sequence 8, Appl
631	4	10.3	40	9	US-09-726-643-94	Sequence 94, Appl
632	4	10.3	40	9	US-09-843-845-13	Sequence 13, Appl
633	4	10.3	40	9	US-09-764-870-511	Sequence 511, App
634	4	10.3	40	9	US-09-864-761-33396	Sequence 33396, A
635	4	10.3	40	9	US-09-864-761-35022	Sequence 35022, A
636	4	10.3	40	9	US-09-864-761-36346	Sequence 36346, A
637	4	10.3	40	9	US-09-864-761-39655	Sequence 39655, A
638	4	10.3	40	9	US-09-864-761-41710	Sequence 41710, A
639	4	10.3	40	9	US-09-864-761-43830	Sequence 43830, A
640	4	10.3	40	9	US-09-864-761-46179	Sequence 46179, A
641	4	10.3	40	9	US-09-925-301-1625	Sequence 1625, Ap
642	4	10.3	40	9	US-09-925-299-1468	Sequence 1468, Ap
643	4	10.3	40	10	US-09-919-473-5	Sequence 5, Appl
644	4	10.3	40	10	US-09-919-473-13	Sequence 13, Appl
645	4	10.3	40	10	US-09-997-498-10	Sequence 10, Appl
646	4	10.3	40	10	US-09-997-498-11	Sequence 11, Appl
647	4	10.3	40	10	US-09-925-300-1113	Sequence 1113, Ap
648	4	10.3	40	11	US-09-818-009-8	Sequence 8, Appl
649	4	10.3	40	11	US-09-925-299-1468	Sequence 1468, Ap
650	4	10.3	40	11	US-09-809-391-535	Sequence 535, App
651	4	10.3	40	11	US-09-852-455-57	Sequence 57, Appl
652	4	10.3	40	11	US-09-948-783-190	Sequence 190, App
653	4	10.3	40	12	US-10-315-964A-2	Sequence 2, Appl
654	4	10.3	40	12	US-10-315-964A-20	Sequence 20, Appl
655	4	10.3	40	12	US-10-315-964A-22	Sequence 22, Appl
656	4	10.3	40	12	US-10-315-964A-173	Sequence 173, App
657	4	10.3	40	12	US-10-315-964A-174	Sequence 174, App
658	4	10.3	40	12	US-10-315-964A-175	Sequence 175, App
659	4	10.3	40	12	US-10-315-964A-176	Sequence 176, App
660	4	10.3	40	12	US-10-315-964A-177	Sequence 177, App
661	4	10.3	40	12	US-10-315-964A-178	Sequence 178, App
662	4	10.3	40	12	US-10-315-964A-179	Sequence 179, App
663	4	10.3	40	12	US-10-315-964A-180	Sequence 180, App
664	4	10.3	40	12	US-10-315-964A-181	Sequence 181, App
665	4	10.3	40	12	US-10-315-964A-182	Sequence 182, App
666	4	10.3	40	12	US-10-315-964A-183	Sequence 183, App
667	4	10.3	40	12	US-10-315-964A-184	Sequence 184, App
668	4	10.3	40	12	US-10-315-964A-185	Sequence 185, App
669	4	10.3	40	12	US-10-315-964A-238	Sequence 238, App
670	4	10.3	40	12	US-10-315-964A-239	Sequence 239, App
671	4	10.3	40	12	US-10-315-964A-242	Sequence 242, App
672	4	10.3	40	12	US-10-315-964A-243	Sequence 243, App
673	4	10.3	40	12	US-10-315-964A-246	Sequence 246, App
674	4	10.3	40	12	US-10-315-964A-247	Sequence 247, App
675	4	10.3	40	12	US-10-315-964A-263	Sequence 263, App
676	4	10.3	40	12	US-10-315-964A-278	Sequence 278, App
677	4	10.3	40	12	US-10-315-964A-321	Sequence 321, App
678	4	10.3	40	12	US-10-315-964A-323	Sequence 323, App
679	4	10.3	40	12	US-10-315-964A-324	Sequence 324, App
680	4	10.3	40	12	US-10-315-964A-326	Sequence 326, App
681	4	10.3	40	12	US-10-315-964A-327	Sequence 327, App
682	4	10.3	40	12	US-10-315-964A-328	Sequence 328, App
683	4	10.3	40	12	US-10-315-964A-329	Sequence 329, App

684	4	10.3	40	12	US-10-315-964A-330	Sequence 330, App
685	4	10.3	40	12	US-10-315-964A-334	Sequence 334, App
686	4	10.3	40	12	US-10-315-964A-335	Sequence 335, App
687	4	10.3	40	12	US-10-315-964A-336	Sequence 336, App
688	4	10.3	40	12	US-10-315-964A-337	Sequence 337, App
689	4	10.3	40	12	US-10-315-964A-338	Sequence 338, App
690	4	10.3	40	12	US-10-315-964A-339	Sequence 339, App
691	4	10.3	40	12	US-10-315-964A-340	Sequence 340, App
692	4	10.3	40	12	US-10-315-964A-341	Sequence 341, App
693	4	10.3	40	12	US-10-315-964A-342	Sequence 342, App
694	4	10.3	40	12	US-10-315-964A-343	Sequence 343, App
695	4	10.3	40	12	US-10-315-964A-345	Sequence 345, App
696	4	10.3	40	12	US-10-315-964A-346	Sequence 346, App
697	4	10.3	40	12	US-10-315-964A-347	Sequence 347, App
698	4	10.3	40	12	US-10-315-964A-351	Sequence 351, App
699	4	10.3	40	12	US-10-315-964A-363	Sequence 363, App
700	4	10.3	40	12	US-10-315-964A-372	Sequence 372, App
701	4	10.3	40	12	US-10-315-964A-374	Sequence 374, App
702	4	10.3	40	12	US-10-315-964A-376	Sequence 376, App
703	4	10.3	40	12	US-10-315-964A-380	Sequence 380, App
704	4	10.3	40	12	US-10-315-964A-382	Sequence 382, App
705	4	10.3	40	12	US-10-315-964A-384	Sequence 384, App
706	4	10.3	40	12	US-10-315-964A-385	Sequence 385, App
707	4	10.3	40	12	US-10-315-964A-386	Sequence 386, App
708	4	10.3	40	12	US-10-315-964A-387	Sequence 387, App
709	4	10.3	40	12	US-10-315-964A-514	Sequence 514, App
710	4	10.3	40	12	US-10-315-964A-515	Sequence 515, App
711	4	10.3	40	12	US-10-315-964A-516	Sequence 516, App
712	4	10.3	40	12	US-10-315-964A-517	Sequence 517, App
713	4	10.3	40	12	US-10-317-251A-2	Sequence 2, Appl
714	4	10.3	40	12	US-10-317-251A-20	Sequence 20, Appl
715	4	10.3	40	12	US-10-317-251A-22	Sequence 22, Appl
716	4	10.3	40	12	US-10-317-251A-173	Sequence 173, App
717	4	10.3	40	12	US-10-317-251A-174	Sequence 174, App
718	4	10.3	40	12	US-10-317-251A-175	Sequence 175, App
719	4	10.3	40	12	US-10-317-251A-176	Sequence 176, App
720	4	10.3	40	12	US-10-317-251A-177	Sequence 177, App
721	4	10.3	40	12	US-10-317-251A-178	Sequence 178, App
722	4	10.3	40	12	US-10-317-251A-179	Sequence 179, App
723	4	10.3	40	12	US-10-317-251A-180	Sequence 180, App
724	4	10.3	40	12	US-10-317-251A-181	Sequence 181, App
725	4	10.3	40	12	US-10-317-251A-182	Sequence 182, App
726	4	10.3	40	12	US-10-317-251A-183	Sequence 183, App
727	4	10.3	40	12	US-10-317-251A-184	Sequence 184, App
728	4	10.3	40	12	US-10-317-251A-185	Sequence 185, App
729	4	10.3	40	12	US-10-317-251A-238	Sequence 238, App
730	4	10.3	40	12	US-10-317-251A-239	Sequence 239, App
731	4	10.3	40	12	US-10-317-251A-242	Sequence 242, App
732	4	10.3	40	12	US-10-317-251A-243	Sequence 243, App
733	4	10.3	40	12	US-10-317-251A-246	Sequence 246, App
734	4	10.3	40	12	US-10-317-251A-247	Sequence 247, App
735	4	10.3	40	12	US-10-317-251A-263	Sequence 263, App
736	4	10.3	40	12	US-10-317-251A-278	Sequence 278, App
737	4	10.3	40	12	US-10-317-251A-321	Sequence 321, App
738	4	10.3	40	12	US-10-317-251A-323	Sequence 323, App
739	4	10.3	40	12	US-10-317-251A-324	Sequence 324, App
740	4	10.3	40	12	US-10-317-251A-326	Sequence 326, App

741	4	10.3	40	12	US-10-317-251A-327	Sequence 327, App
742	4	10.3	40	12	US-10-317-251A-328	Sequence 328, App
743	4	10.3	40	12	US-10-317-251A-329	Sequence 329, App
744	4	10.3	40	12	US-10-317-251A-330	Sequence 330, App
745	4	10.3	40	12	US-10-317-251A-334	Sequence 334, App
746	4	10.3	40	12	US-10-317-251A-335	Sequence 335, App
747	4	10.3	40	12	US-10-317-251A-336	Sequence 336, App
748	4	10.3	40	12	US-10-317-251A-337	Sequence 337, App
749	4	10.3	40	12	US-10-317-251A-338	Sequence 338, App
750	4	10.3	40	12	US-10-317-251A-339	Sequence 339, App
751	4	10.3	40	12	US-10-317-251A-340	Sequence 340, App
752	4	10.3	40	12	US-10-317-251A-341	Sequence 341, App
753	4	10.3	40	12	US-10-317-251A-342	Sequence 342, App
754	4	10.3	40	12	US-10-317-251A-343	Sequence 343, App
755	4	10.3	40	12	US-10-317-251A-345	Sequence 345, App
756	4	10.3	40	12	US-10-317-251A-346	Sequence 346, App
757	4	10.3	40	12	US-10-317-251A-347	Sequence 347, App
758	4	10.3	40	12	US-10-317-251A-351	Sequence 351, App
759	4	10.3	40	12	US-10-317-251A-363	Sequence 363, App
760	4	10.3	40	12	US-10-317-251A-372	Sequence 372, App
761	4	10.3	40	12	US-10-317-251A-374	Sequence 374, App
762	4	10.3	40	12	US-10-317-251A-376	Sequence 376, App
763	4	10.3	40	12	US-10-317-251A-380	Sequence 380, App
764	4	10.3	40	12	US-10-317-251A-382	Sequence 382, App
765	4	10.3	40	12	US-10-317-251A-384	Sequence 384, App
766	4	10.3	40	12	US-10-317-251A-385	Sequence 385, App
767	4	10.3	40	12	US-10-317-251A-386	Sequence 386, App
768	4	10.3	40	12	US-10-317-251A-387	Sequence 387, App
769	4	10.3	40	12	US-10-317-251A-514	Sequence 514, App
770	4	10.3	40	12	US-10-317-251A-515	Sequence 515, App
771	4	10.3	40	12	US-10-317-251A-516	Sequence 516, App
772	4	10.3	40	12	US-10-317-251A-517	Sequence 517, App
773	4	10.3	40	12	US-10-317-252A-2	Sequence 2, Appl
774	4	10.3	40	12	US-10-317-252A-20	Sequence 20, Appl
775	4	10.3	40	12	US-10-317-252A-22	Sequence 22, Appl
776	4	10.3	40	12	US-10-317-252A-173	Sequence 173, App
777	4	10.3	40	12	US-10-317-252A-174	Sequence 174, App
778	4	10.3	40	12	US-10-317-252A-175	Sequence 175, App
779	4	10.3	40	12	US-10-317-252A-176	Sequence 176, App
780	4	10.3	40	12	US-10-317-252A-177	Sequence 177, App
781	4	10.3	40	12	US-10-317-252A-178	Sequence 178, App
782	4	10.3	40	12	US-10-317-252A-179	Sequence 179, App
783	4	10.3	40	12	US-10-317-252A-180	Sequence 180, App
784	4	10.3	40	12	US-10-317-252A-181	Sequence 181, App
785	4	10.3	40	12	US-10-317-252A-182	Sequence 182, App
786	4	10.3	40	12	US-10-317-252A-183	Sequence 183, App
787	4	10.3	40	12	US-10-317-252A-184	Sequence 184, App
788	4	10.3	40	12	US-10-317-252A-185	Sequence 185, App
789	4	10.3	40	12	US-10-317-252A-238	Sequence 238, App
790	4	10.3	40	12	US-10-317-252A-239	Sequence 239, App
791	4	10.3	40	12	US-10-317-252A-242	Sequence 242, App
792	4	10.3	40	12	US-10-317-252A-243	Sequence 243, App
793	4	10.3	40	12	US-10-317-252A-246	Sequence 246, App
794	4	10.3	40	12	US-10-317-252A-247	Sequence 247, App
795	4	10.3	40	12	US-10-317-252A-263	Sequence 263, App
796	4	10.3	40	12	US-10-317-252A-278	Sequence 278, App
797	4	10.3	40	12	US-10-317-252A-321	Sequence 321, App

798	4	10.3	40	12	US-10-317-252A-323	Sequence 323, App
799	4	10.3	40	12	US-10-317-252A-324	Sequence 324, App
800	4	10.3	40	12	US-10-317-252A-326	Sequence 326, App
801	4	10.3	40	12	US-10-317-252A-327	Sequence 327, App
802	4	10.3	40	12	US-10-317-252A-328	Sequence 328, App
803	4	10.3	40	12	US-10-317-252A-329	Sequence 329, App
804	4	10.3	40	12	US-10-317-252A-330	Sequence 330, App
805	4	10.3	40	12	US-10-317-252A-334	Sequence 334, App
806	4	10.3	40	12	US-10-317-252A-335	Sequence 335, App
807	4	10.3	40	12	US-10-317-252A-336	Sequence 336, App
808	4	10.3	40	12	US-10-317-252A-337	Sequence 337, App
809	4	10.3	40	12	US-10-317-252A-338	Sequence 338, App
810	4	10.3	40	12	US-10-317-252A-339	Sequence 339, App
811	4	10.3	40	12	US-10-317-252A-340	Sequence 340, App
812	4	10.3	40	12	US-10-317-252A-341	Sequence 341, App
813	4	10.3	40	12	US-10-317-252A-342	Sequence 342, App
814	4	10.3	40	12	US-10-317-252A-343	Sequence 343, App
815	4	10.3	40	12	US-10-317-252A-345	Sequence 345, App
816	4	10.3	40	12	US-10-317-252A-346	Sequence 346, App
817	4	10.3	40	12	US-10-317-252A-347	Sequence 347, App
818	4	10.3	40	12	US-10-317-252A-351	Sequence 351, App
819	4	10.3	40	12	US-10-317-252A-363	Sequence 363, App
820	4	10.3	40	12	US-10-317-252A-372	Sequence 372, App
821	4	10.3	40	12	US-10-317-252A-374	Sequence 374, App
822	4	10.3	40	12	US-10-317-252A-376	Sequence 376, App
823	4	10.3	40	12	US-10-317-252A-380	Sequence 380, App
824	4	10.3	40	12	US-10-317-252A-382	Sequence 382, App
825	4	10.3	40	12	US-10-317-252A-384	Sequence 384, App
826	4	10.3	40	12	US-10-317-252A-385	Sequence 385, App
827	4	10.3	40	12	US-10-317-252A-386	Sequence 386, App
828	4	10.3	40	12	US-10-317-252A-387	Sequence 387, App
829	4	10.3	40	12	US-10-317-252A-514	Sequence 514, App
830	4	10.3	40	12	US-10-317-252A-515	Sequence 515, App
831	4	10.3	40	12	US-10-317-252A-516	Sequence 516, App
832	4	10.3	40	12	US-10-317-252A-517	Sequence 517, App
833	4	10.3	40	12	US-10-032-201B-111	Sequence 111, App
834	4	10.3	40	12	US-10-346-802-11	Sequence 11, Appl
835	4	10.3	40	12	US-09-882-171-535	Sequence 535, App
836	4	10.3	40	12	US-10-331-907-14	Sequence 14, Appl
837	4	10.3	40	12	US-10-106-588-10	Sequence 10, Appl
838	4	10.3	40	12	US-10-106-588-11	Sequence 11, Appl
839	4	10.3	40	12	US-10-029-386-28802	Sequence 28802, A
840	4	10.3	40	12	US-10-029-386-29123	Sequence 29123, A
841	4	10.3	40	12	US-10-062-599-140	Sequence 140, App
842	4	10.3	40	12	US-10-264-049-2494	Sequence 2494, Ap
843	4	10.3	40	14	US-10-042-417-67	Sequence 67, Appl
844	4	10.3	40	14	US-10-042-141-94	Sequence 94, Appl
845	4	10.3	40	15	US-10-099-766-14	Sequence 14, Appl
846	4	10.3	40	15	US-10-099-766-15	Sequence 15, Appl
847	4	10.3	40	15	US-10-012-542-312	Sequence 312, App
848	4	10.3	40	15	US-10-125-540-511	Sequence 511, App
849	4	10.3	40	15	US-10-062-831-140	Sequence 140, App
850	4	10.3	40	15	US-10-106-698-6428	Sequence 6428, Ap
851	4	10.3	40	15	US-10-106-698-6529	Sequence 6529, Ap
852	4	10.3	40	15	US-10-197-954-140	Sequence 140, App
853	3	7.7	28	8	US-08-424-550B-202	Sequence 202, App
854	3	7.7	28	8	US-08-908-884-6	Sequence 6, Appl

855	3	7.7	28	8	US-08-488-123-10	Sequence 10, Appl
856	3	7.7	28	9	US-09-157-748-4	Sequence 4, Appli
857	3	7.7	28	9	US-09-799-983-15	Sequence 15, Appl
858	3	7.7	28	9	US-09-846-258-8	Sequence 8, Appli
859	3	7.7	28	9	US-09-838-785-25	Sequence 25, Appl
860	3	7.7	28	9	US-09-904-380-30	Sequence 30, Appl
861	3	7.7	28	9	US-09-895-072-27	Sequence 27, Appl
862	3	7.7	28	9	US-09-848-035-10	Sequence 10, Appl
863	3	7.7	28	9	US-09-848-164-105	Sequence 105, App
864	3	7.7	28	9	US-09-864-761-33771	Sequence 33771, A
865	3	7.7	28	9	US-09-864-761-33837	Sequence 33837, A
866	3	7.7	28	9	US-09-864-761-34318	Sequence 34318, A
867	3	7.7	28	9	US-09-864-761-34965	Sequence 34965, A
868	3	7.7	28	9	US-09-864-761-34971	Sequence 34971, A
869	3	7.7	28	9	US-09-864-761-35098	Sequence 35098, A
870	3	7.7	28	9	US-09-864-761-35107	Sequence 35107, A
871	3	7.7	28	9	US-09-864-761-35219	Sequence 35219, A
872	3	7.7	28	9	US-09-864-761-35515	Sequence 35515, A
873	3	7.7	28	9	US-09-864-761-35640	Sequence 35640, A
874	3	7.7	28	9	US-09-864-761-35924	Sequence 35924, A
875	3	7.7	28	9	US-09-864-761-36085	Sequence 36085, A
876	3	7.7	28	9	US-09-864-761-36747	Sequence 36747, A
877	3	7.7	28	9	US-09-864-761-37130	Sequence 37130, A
878	3	7.7	28	9	US-09-864-761-37208	Sequence 37208, A
879	3	7.7	28	9	US-09-864-761-37728	Sequence 37728, A
880	3	7.7	28	9	US-09-864-761-37923	Sequence 37923, A
881	3	7.7	28	9	US-09-864-761-39731	Sequence 39731, A
882	3	7.7	28	9	US-09-864-761-39822	Sequence 39822, A
883	3	7.7	28	9	US-09-864-761-39959	Sequence 39959, A
884	3	7.7	28	9	US-09-864-761-40184	Sequence 40184, A
885	3	7.7	28	9	US-09-864-761-40236	Sequence 40236, A
886	3	7.7	28	9	US-09-864-761-40453	Sequence 40453, A
887	3	7.7	28	9	US-09-864-761-40487	Sequence 40487, A
888	3	7.7	28	9	US-09-864-761-40663	Sequence 40663, A
889	3	7.7	28	9	US-09-864-761-41015	Sequence 41015, A
890	3	7.7	28	9	US-09-864-761-41604	Sequence 41604, A
891	3	7.7	28	9	US-09-864-761-42008	Sequence 42008, A
892	3	7.7	28	9	US-09-864-761-42022	Sequence 42022, A
893	3	7.7	28	9	US-09-864-761-42080	Sequence 42080, A
894	3	7.7	28	9	US-09-864-761-42292	Sequence 42292, A
895	3	7.7	28	9	US-09-864-761-42456	Sequence 42456, A
896	3	7.7	28	9	US-09-864-761-42519	Sequence 42519, A
897	3	7.7	28	9	US-09-864-761-42702	Sequence 42702, A
898	3	7.7	28	9	US-09-864-761-42930	Sequence 42930, A
899	3	7.7	28	9	US-09-864-761-43955	Sequence 43955, A
900	3	7.7	28	9	US-09-864-761-44205	Sequence 44205, A
901	3	7.7	28	9	US-09-864-761-44241	Sequence 44241, A
902	3	7.7	28	9	US-09-864-761-44249	Sequence 44249, A
903	3	7.7	28	9	US-09-864-761-44625	Sequence 44625, A
904	3	7.7	28	9	US-09-864-761-44626	Sequence 44626, A
905	3	7.7	28	9	US-09-864-761-44688	Sequence 44688, A
906	3	7.7	28	9	US-09-864-761-44806	Sequence 44806, A
907	3	7.7	28	9	US-09-864-761-44899	Sequence 44899, A
908	3	7.7	28	9	US-09-864-761-45102	Sequence 45102, A
909	3	7.7	28	9	US-09-864-761-45199	Sequence 45199, A
910	3	7.7	28	9	US-09-864-761-45427	Sequence 45427, A
911	3	7.7	28	9	US-09-864-761-45563	Sequence 45563, A

912	3	7.7	28	9	US-09-864-761-46316	Sequence 46316, A
913	3	7.7	28	9	US-09-864-761-46365	Sequence 46365, A
914	3	7.7	28	9	US-09-864-761-46937	Sequence 46937, A
915	3	7.7	28	9	US-09-864-761-47458	Sequence 47458, A
916	3	7.7	28	9	US-09-864-761-47891	Sequence 47891, A
917	3	7.7	28	9	US-09-864-761-48171	Sequence 48171, A
918	3	7.7	28	9	US-09-864-761-48752	Sequence 48752, A
919	3	7.7	28	9	US-09-864-761-48764	Sequence 48764, A
920	3	7.7	28	9	US-09-815-242-12924	Sequence 12924, A
921	3	7.7	28	9	US-09-815-242-13123	Sequence 13123, A
922	3	7.7	28	9	US-09-728-721-21	Sequence 21, Appl
923	3	7.7	28	9	US-09-728-721-22	Sequence 22, Appl
924	3	7.7	28	9	US-09-728-721-23	Sequence 23, Appl
925	3	7.7	28	9	US-09-782-980-144	Sequence 144, App
926	3	7.7	28	9	US-09-782-980-164	Sequence 164, App
927	3	7.7	28	9	US-09-782-980-165	Sequence 165, App
928	3	7.7	28	9	US-09-908-323-6	Sequence 6, Appli
929	3	7.7	28	9	US-09-815-626-11	Sequence 11, Appl
930	3	7.7	28	9	US-09-879-666-4	Sequence 4, Appli
931	3	7.7	28	9	US-09-737-379-4	Sequence 4, Appli
932	3	7.7	28	9	US-09-737-379-9	Sequence 9, Appli
933	3	7.7	28	9	US-09-920-552-48	Sequence 48, Appl
934	3	7.7	28	9	US-09-796-744-2	Sequence 2, Appli
935	3	7.7	28	9	US-09-929-818-1	Sequence 1, Appli
936	3	7.7	28	9	US-09-929-818-2	Sequence 2, Appli
937	3	7.7	28	9	US-09-929-818-3	Sequence 3, Appli
938	3	7.7	28	9	US-09-929-818-4	Sequence 4, Appli
939	3	7.7	28	9	US-09-929-818-5	Sequence 5, Appli
940	3	7.7	28	9	US-09-929-818-6	Sequence 6, Appli
941	3	7.7	28	9	US-09-929-818-7	Sequence 7, Appli
942	3	7.7	28	9	US-09-929-818-10	Sequence 10, Appl
943	3	7.7	28	9	US-09-929-818-11	Sequence 11, Appl
944	3	7.7	28	9	US-09-929-818-12	Sequence 12, Appl
945	3	7.7	28	9	US-09-929-818-13	Sequence 13, Appl
946	3	7.7	28	9	US-09-929-818-14	Sequence 14, Appl
947	3	7.7	28	9	US-09-929-818-15	Sequence 15, Appl
948	3	7.7	28	9	US-09-929-818-16	Sequence 16, Appl
949	3	7.7	28	9	US-09-929-818-17	Sequence 17, Appl
950	3	7.7	28	9	US-09-929-818-18	Sequence 18, Appl
951	3	7.7	28	9	US-09-929-818-19	Sequence 19, Appl
952	3	7.7	28	9	US-09-929-818-21	Sequence 21, Appl
953	3	7.7	28	9	US-09-929-818-22	Sequence 22, Appl
954	3	7.7	28	9	US-09-929-818-26	Sequence 26, Appl
955	3	7.7	28	9	US-09-929-818-27	Sequence 27, Appl
956	3	7.7	28	9	US-09-929-818-28	Sequence 28, Appl
957	3	7.7	28	9	US-09-929-818-29	Sequence 29, Appl
958	3	7.7	28	9	US-09-929-818-30	Sequence 30, Appl
959	3	7.7	28	9	US-09-929-818-31	Sequence 31, Appl
960	3	7.7	28	9	US-09-929-818-32	Sequence 32, Appl
961	3	7.7	28	9	US-09-929-818-33	Sequence 33, Appl
962	3	7.7	28	9	US-09-929-818-34	Sequence 34, Appl
963	3	7.7	28	9	US-09-929-818-35	Sequence 35, Appl
964	3	7.7	28	9	US-09-929-818-36	Sequence 36, Appl
965	3	7.7	28	9	US-09-929-818-37	Sequence 37, Appl
966	3	7.7	28	9	US-09-929-818-38	Sequence 38, Appl
967	3	7.7	28	9	US-09-929-818-39	Sequence 39, Appl
968	3	7.7	28	9	US-09-929-818-40	Sequence 40, Appl

969	3	7.7	28	9	US-09-929-818-41	Sequence 41, Appl
970	3	7.7	28	9	US-09-929-818-43	Sequence 43, Appl
971	3	7.7	28	9	US-09-929-818-44	Sequence 44, Appl
972	3	7.7	28	9	US-09-929-818-45	Sequence 45, Appl
973	3	7.7	28	9	US-09-929-818-46	Sequence 46, Appl
974	3	7.7	28	9	US-09-929-818-47	Sequence 47, Appl
975	3	7.7	28	9	US-09-929-818-48	Sequence 48, Appl
976	3	7.7	28	9	US-09-929-818-49	Sequence 49, Appl
977	3	7.7	28	9	US-09-929-818-50	Sequence 50, Appl
978	3	7.7	28	9	US-09-929-818-51	Sequence 51, Appl
979	3	7.7	28	9	US-09-929-818-52	Sequence 52, Appl
980	3	7.7	28	9	US-09-929-818-53	Sequence 53, Appl
981	3	7.7	28	9	US-09-929-818-54	Sequence 54, Appl
982	3	7.7	28	9	US-09-929-818-61	Sequence 61, Appl
983	3	7.7	28	9	US-09-929-818-62	Sequence 62, Appl
984	3	7.7	28	9	US-09-929-818-66	Sequence 66, Appl
985	3	7.7	28	9	US-09-929-818-69	Sequence 69, Appl
986	3	7.7	28	9	US-09-929-818-76	Sequence 76, Appl
987	3	7.7	28	9	US-09-929-818-77	Sequence 77, Appl
988	3	7.7	28	9	US-09-929-818-80	Sequence 80, Appl
989	3	7.7	28	9	US-09-929-818-87	Sequence 87, Appl
990	3	7.7	28	9	US-09-929-818-94	Sequence 94, Appl
991	3	7.7	28	9	US-09-929-818-95	Sequence 95, Appl
992	3	7.7	28	9	US-09-929-818-97	Sequence 97, Appl
993	3	7.7	28	9	US-09-929-818-99	Sequence 99, Appl
994	3	7.7	28	9	US-09-929-818-100	Sequence 100, App
995	3	7.7	28	9	US-09-929-818-101	Sequence 101, App
996	3	7.7	28	9	US-09-929-818-102	Sequence 102, App
997	3	7.7	28	9	US-09-929-818-103	Sequence 103, App
998	3	7.7	28	9	US-09-929-818-104	Sequence 104, App
999	3	7.7	28	9	US-09-929-818-105	Sequence 105, App
1000	3	7.7	28	15	US-10-216-209-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
 US-09-843-221A-160
 ; Sequence 160, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUIK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE-
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27

; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 160
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TIP39

US-09-843-221A-160

Query Match 100.0%; Score 39; DB 11; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

RESULT 2

US-09-843-221A-170

; Sequence 170, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENIUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - TIP39
; NAME/KEY: misc_feature
; LOCATION: (39)..(39)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus

US-09-843-221A-170

Query Match 100.0%; Score 39; DB 11; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

RESULT 3

US-10-014-162-1

; Sequence 1, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Bos taurus

US-10-014-162-1

Query Match 100.0%; Score 39; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

RESULT 4

US-10-014-162-2

; Sequence 2, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Bos taurus

US-10-014-162-2

Query Match 97.4%; Score 38; DB 15; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 LALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 38

RESULT 5

US-10-014-162-38

; Sequence 38, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-38

Query Match 97.4%; Score 38; DB 15; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDA 38
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDA 38

RESULT 6

US-10-014-162-3

; Sequence 3, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335

; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-3

Query Match 94.9%; Score 37; DB 15; Length 37;
Best Local Similarity 100.0%; Pred. No. 8.5e-27;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 37

RESULT 7

US-10-014-162-39

; Sequence 39, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-39

Query Match 94.9%; Score 37; DB 15; Length 37;
Best Local Similarity 100.0%; Pred. No. 8.5e-27;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLD 37
||| ||| ||| ||| ||| ||| ||| |||
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLD 37

RESULT 8

US-10-014-162-4

; Sequence 4, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.

; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-4

Query Match 92.3%; Score 36; DB 15; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.7e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 LADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 36

RESULT 9

US-10-014-162-40
; Sequence 40, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-40

Query Match 92.3%; Score 36; DB 15; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.7e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIALADDAAFRERARLLAALERRHWLNSYMHKLLVL 36
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 SIALADDAAFRERARLLAALERRHWLNSYMHKLLVL 36

RESULT 10
US-10-014-162-5
; Sequence 5, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-5

```

Query Match           89.7%;  Score 35;  DB 15;  Length 35;
Best Local Similarity 100.0%;  Pred. No. 5.3e-25;
Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 ADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
        ||||||| | | | | | | | | | | | | | | | | |
Db      1 ADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 35

```

RESULT 11
US-10-014-162-41
; Sequence 41, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-41

Query Match 89.7%; Score 35; DB 15; Length 35;
Best Local Similarity 100.0%; Pred. No. 5.3e-25;

; LENGTH: 34
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-42

Query Match 87.2%; Score 34; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.2e-24;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLL 34
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLL 34

RESULT 14
US-10-014-162-7
; Sequence 7, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-7

Query Match 84.6%; Score 33; DB 15; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.3e-23;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DAAFGERARLLAALERRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAAFGERARLLAALERRHWLNSYMHKLLVLDAP 33

RESULT 15
US-10-014-162-43
; Sequence 43, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11

; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-43

Query Match 84.6%; Score 33; DB 15; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.3e-23;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHKL 33
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHKL 33

RESULT 16

US-10-014-162-8

; Sequence 8, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-8

Query Match 82.1%; Score 32; DB 15; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AAFRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 AAFRERARLLAALERRHWLNSYMHKLLVLDAP 32

RESULT 17

US-10-014-162-44

; Sequence 44, Application US/10014162
; Publication No. US20030032096A1

; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-44

Query Match 82.1%; Score 32; DB 15; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNSYMHK 32
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 SLALADDAAFRERARLLAALERRHWLNSYMHK 32

RESULT 18

US-10-014-162-9
; Sequence 9, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-9

Query Match 79.5%; Score 31; DB 15; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.1e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AFRERARLLAALERRHWLNSYMHKLLVLDAP 39
|||||||||||||||||||||||||||

Query Match 79.5%; Score 31; DB 15; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.1e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AFRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| ||| ||| |||
Db 1 AFRERARLLAALERRHWLNSYMHKLLVLDAP 31

RESULT 21

US-10-014-162-10
; Sequence 10, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Bos taurus

US-10-014-162-10

Query Match 76.9%; Score 30; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 FRERARLLAALERRHWLNSYMHKLLVLDAP 39
||| ||| ||| ||| ||| |||
Db 1 FRERARLLAALERRHWLNSYMHKLLVLDAP 30

RESULT 22

US-10-014-162-46
; Sequence 46, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15

; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-46

Query Match 76.9%; Score 30; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRH WLNSYM 30
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SLALADDAAFRERARLLAALERRH WLNSYM 30

RESULT 23

US-10-014-162-79

; Sequence 79, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-79

Query Match 76.9%; Score 30; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 FRERARLLAALERRH WLNSYMHKLLVLDAP 39
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 FRERARLLAALERRH WLNSYMHKLLVLDAP 30

RESULT 24

US-10-014-162-11

; Sequence 11, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS

; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-11

Query Match 74.4%; Score 29; DB 15; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 RERARLLAALERRHWLNSYMHKLLVLDAP 39
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 RERARLLAALERRHWLNSYMHKLLVLDAP 29

RESULT 25
US-10-014-162-47
; Sequence 47, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-47

Query Match 74.4%; Score 29; DB 15; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SLALADDAAFRERARLLAALERRHWLNSY 29
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SLALADDAAFRERARLLAALERRHWLNSY 29

RESULT 26

US-10-014-162-80
; Sequence 80, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-80

Query Match 74.4%; Score 29; DB 15; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERARLLAALERRHWLNSYMHKLLVLDAP 39
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 RERARLLAALERRHWLNSYMHKLLVLDAP 29

RESULT 27
US-10-014-162-48
; Sequence 48, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-48

Query Match 71.8%; Score 28; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALADDAAFRERARLLAALERRHWLNS 28
|||
Db 1 SLALADDAAFRERARLLAALERRHWLNS 28

RESULT 28

US-10-154-884B-11122

; Sequence 11122, Application US/10154884B

; Publication No. US20040005561A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algaté, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc W.

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy of

; TITLE OF INVENTION: Hematological Malignancies

; FILE REFERENCE: 014058-013521US

; CURRENT APPLICATION NUMBER: US/10/154,884B

; CURRENT FILING DATE: 2002-05-23

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: US 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 60/222,903

; PRIOR FILING DATE: 2000-08-03

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 11290

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 11122

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-154-884B-11122

Query Match 15.4%; Score 6; DB 12; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AALERR 23

|||||

Db 3 AALERR 8

RESULT 29
US-10-154-884B-11106
; Sequence 11106, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy of
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11106
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11106

Query Match 15.4%; Score 6; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AALERR 23

|||||

Db 3 AALERR 8

RESULT 30
US-10-026-741-7
; Sequence 7, Application US/10026741
; Publication No. US20030049604A1
; GENERAL INFORMATION:
; APPLICANT: CHARNEAU, PIERRE
; CLAVEL, FRANCOISE
; BORMAN, ANDREW
; QUILLENT, CAROLINE
; GUETARD, DENISE
; MONTAGNIER, LUC
; DONJON DE SAINT-MARTIN, JACQUELINE
; COHEN, JAQUES
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
; SUBTYPE) ANTIGENS
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/026,741
; FILING DATE: 27-Dec-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/817,441
; FILING DATE: 31-AUG-1998
; APPLICATION NUMBER: PCT/FR 95/01391
; FILING DATE: 20-OCT-1995
; APPLICATION NUMBER: FR 9412554
; FILING DATE: 20-OCT-1994
; APPLICATION NUMBER: FR 9502526
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03260.6005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-026-741-7

Query Match 15.4%; Score 6; DB 15; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
|||||
Db 1 RARLLA 6

RESULT 31

US-09-779-451-40
; Sequence 40, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (18)..(18)
; OTHER INFORMATION: May be any amino acid

US-09-779-451-40

Query Match 15.4%; Score 6; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLLA 18
|||||
Db 25 RARLLA 30

RESULT 32

US-09-864-761-37845
; Sequence 37845, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37845
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL031665.18
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
; OTHER INFORMATION: EST_HUMAN HIT: AV709682.1, EVALUE 4.00e-03
US-09-864-761-37845

Query Match 12.8%; Score 5; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLL 17
|||||
Db 20 RARLL 24

RESULT 33

US-09-864-761-38197

; Sequence 38197, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES

USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 38197
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL109809.14
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
OTHER INFORMATION: EST_HUMAN HIT: BE514786.1, EVALUE 2.70e-02
US-09-864-761-38197

Query Match 12.8%; Score 5; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLL 17
|||||
Db 13 RARLL 17

RESULT 34
US-09-864-761-45958
; Sequence 45958, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45958
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL109809.18
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.65
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.9
; OTHER INFORMATION: EST_HUMAN HIT: BE514786.1, EVALUE 4.00e-01
US-09-864-761-45958

Query Match 12.8%; Score 5; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLL 17
|||
Db 15 RARLL 19

RESULT 35
US-09-782-980-145
; Sequence 145, Application US/09782980

; Patent No. US20020072089A1
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran M.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Busfield, Samantha J.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gu, Wei
; APPLICANT: White, David
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND
; TITLE OF INVENTION: STMST PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI-121CP
; CURRENT APPLICATION NUMBER: US/09/782,980
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US00/02125
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/448,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/276,400
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: 60/117,580
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,195
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/014,348
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/086,892
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/296,208
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 09/063,950
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 09/561,381
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,810
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/087,121
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/672,721
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/049,799
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-980-145

Query Match 12.8%; Score 5; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

|||||
7 LALAD 11

RESULT 36
US-09-776-724A-114
; Sequence 114, Application US/09776724A
; Publication No. US20030050455A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 64 Human Secreted Proteins
; FILE REFERENCE: PZ011
; CURRENT APPLICATION NUMBER: US/09/776,724A
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/180,909
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 09/669,688
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/229,982
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: PCT/US98/14613
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/052,661
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,872
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,871
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,874
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,873
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,870
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,875
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/053,440
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,441
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,442
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/056,359
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,725
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,985
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,952
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,989
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056,361
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,726
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,724

; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,946
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,683
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-776-724A-114

Query Match 12.8%; Score 5; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 KLLVL 36
|||||
Db 7 KLLVL 11

RESULT 37
US-10-001-887-123
; Sequence 123, Application US/10001887
; Publication No. US20020155464A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Cafferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Proteins
; FILE REFERENCE: DEX-0269
; CURRENT APPLICATION NUMBER: US/10/001,887
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/249,998
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/252,563
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-887-123

Query Match 12.8%; Score 5; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 KLLVL 36
|||||
Db 8 KLLVL 12

RESULT 38

US-09-905-831-12

; Sequence 12, Application US/09905831

; Patent No. US20020119572A1

; GENERAL INFORMATION:

; APPLICANT: Jacobson, Joseph

; APPLICANT: Schwartz, John

; APPLICANT: Hamad, Kimberly

; APPLICANT: Zhang, Shuguang

; TITLE OF INVENTION: Direct, Externally Imposed Control of Polypeptides

; FILE REFERENCE: MLB-086

; CURRENT APPLICATION NUMBER: US/09/905,831

; CURRENT FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/276,313

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: US 60/218,312

; PRIOR FILING DATE: 2000-07-14

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 12

; LENGTH: 29

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: dCoil-adIL29 dimeric coiled coil

US-09-905-831-12

Query Match 12.8%; Score 5; DB 10; Length 29;

Best Local Similarity 100.0%; Pred. No. 9.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAALE 21

|||||

Db 9 LAALE 13

RESULT 39

US-09-905-831-14

; Sequence 14, Application US/09905831

; Patent No. US20020119572A1

; GENERAL INFORMATION:

; APPLICANT: Jacobson, Joseph

; APPLICANT: Schwartz, John

; APPLICANT: Hamad, Kimberly

; APPLICANT: Zhang, Shuguang

; TITLE OF INVENTION: Direct, Externally Imposed Control of Polypeptides

; FILE REFERENCE: MLB-086

; CURRENT APPLICATION NUMBER: US/09/905,831

; CURRENT FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/276,313

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: US 60/218,312

; PRIOR FILING DATE: 2000-07-14

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 14
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: dCoil-LA29 dimeric coiled coil
US-09-905-831-14

Query Match 12.8%; Score 5; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAALE 21
|||||
Db 2 LAALE 6

RESULT 40

US-09-905-831-15

; Sequence 15, Application US/09905831
; Patent No. US20020119572A1
; GENERAL INFORMATION:
; APPLICANT: Jacobson, Joseph
; APPLICANT: Schwartz, John
; APPLICANT: Hamad, Kimberly
; APPLICANT: Zhang, Shuguang
; TITLE OF INVENTION: Direct, Externally Imposed Control of Polypeptides
; FILE REFERENCE: MLB-086
; CURRENT APPLICATION NUMBER: US/09/905,831
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/276,313
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/218,312
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: tCoil-LL29 trimeric bundle
US-09-905-831-15

Query Match 12.8%; Score 5; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAALE 21
|||||
Db 9 LAALE 13

Search completed: January 14, 2004, 11:15:12
Job time : 27.243 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 29.1589 Seconds
(without alignments)
345.145 Million cell updates/sec

Title: US-09-843-221A-170
Perfect score: 39
Sequence: 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 13497

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SPTREMBL_23:
1: sp_archea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rat:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match Length	DB	ID	Description
---------------	-------	-----------------------	----	----	-------------

1	6	15.4	37	16	Q8P6H8	Q8p6h8 xanthomonas
2	6	15.4	38	16	Q8FVK2	Q8fvk2 brucella su
3	5	12.8	28	5	Q9TWE2	Q9twe2 paracentrot
4	5	12.8	28	11	Q9WTS1	Q9wts1 rattus norv
5	5	12.8	29	6	Q9TP2	Q9ttp2 pan troglod
6	5	12.8	29	11	Q9JLR6	Q9jlr6 rattus norv
7	5	12.8	29	16	Q9I390	Q9i390 pseudomonas
8	5	12.8	31	2	Q9RHF9	Q9rhf9 acinetobact
9	5	12.8	31	9	Q9T1K0	Q9t1k0 bacteriopha
10	5	12.8	31	9	Q9T1K2	Q9t1k2 bacteriopha
11	5	12.8	31	9	Q9T1K1	Q9t1k3 bacteriopha
12	5	12.8	31	9	Q9T1K3	Q9km83 vibrio chol
13	5	12.8	33	16	Q9KM83	Q8xy48 ralstonia s
14	5	12.8	33	16	Q8XY48	Q27372 bombyx mori
15	5	12.8	37	5	Q27372	Q8syh5 drosophila
16	5	12.8	37	5	Q8SYH5	Q9ttr4 cercopithec
17	5	12.8	37	6	Q9TTR4	Q9n260 sus scrofa
18	5	12.8	37	6	Q9N260	Q9h4y8 homo sapien
19	5	12.8	38	4	Q9H4Y8	Q8u580 agrobacteri
20	5	12.8	38	16	Q8U580	Q9lb47 helicobacte
21	5	12.8	39	2	Q9LB47	Q9udi2 homo sapien
22	5	12.8	39	4	Q9UDI2	O61645 aplysia cal
23	5	12.8	39	5	O61645	Q9zxk1 bacteriopha
24	5	12.8	39	9	Q9ZXK1	Q9zry5 prunus aviu
25	5	12.8	39	10	Q9ZRY5	Q9pxwl simian immu
26	5	12.8	39	15	Q9PXW1	Q8f6j1 leptospira
27	5	12.8	39	16	Q8F6J1	Q8nhyl homo sapien
28	4	10.3	28	4	Q8NHY1	Q8mjg7 sus scrofa
29	4	10.3	28	6	Q8MJG7	Q95l33 equus cabal
30	4	10.3	28	6	Q95L33	P92760 uromastyx a
31	4	10.3	28	8	P92760	Q9qvc9 rattus sp.
32	4	10.3	28	11	Q9QVC9	Q62677 rattus norv
33	4	10.3	28	11	Q62677	Q8tgg9 saccharomyc
34	4	10.3	29	3	Q8TGG9	Q9br24 homo sapien
35	4	10.3	29	4	Q9BR24	Q9ubw6 homo sapien
36	4	10.3	29	4	Q9UBW6	Q9ucw5 homo sapien
37	4	10.3	29	4	Q9UCW5	Q9bm71 lasius nige
38	4	10.3	29	5	Q9BM71	Q29891 homo sapien
39	4	10.3	29	7	Q29891	O19668 homo sapien
40	4	10.3	29	7	O19668	Q30141 homo sapien
41	4	10.3	29	7	Q30141	O19735 homo sapien
42	4	10.3	29	7	O19735	Q29807 homo sapien
43	4	10.3	29	7	Q29807	O19733 homo sapien
44	4	10.3	29	7	O19733	Q29892 homo sapien
45	4	10.3	29	7	Q29892	O19661 homo sapien
46	4	10.3	29	7	O19661	O19663 homo sapien
47	4	10.3	29	7	O19663	O19737 homo sapien
48	4	10.3	29	7	O19737	O19665 homo sapien
49	4	10.3	29	7	O19665	Q29815 homo sapien
50	4	10.3	29	7	Q29815	O19734 homo sapien
51	4	10.3	29	7	O19734	O19662 homo sapien
52	4	10.3	29	7	O19662	Q30138 homo sapien
53	4	10.3	29	7	Q30138	O19731 homo sapien
54	4	10.3	29	7	O19731	O19681 homo sapien
55	4	10.3	29	7	O19681	O19666 homo sapien
56	4	10.3	29	7	O19666	Q30140 homo sapien
57	4	10.3	29	7	Q30140	

58	4	10.3	29	7	Q06662	Q06662 homo sapien
59	4	10.3	29	7	Q06654	Q06654 homo sapien
60	4	10.3	29	7	Q06664	Q06664 homo sapien
61	4	10.3	29	7	Q29808	Q29808 homo sapien
62	4	10.3	29	7	Q06663	Q06663 homo sapien
63	4	10.3	29	8	Q9G651	Q9g651 otocryptis
64	4	10.3	29	11	Q9R1N7	Q9r1n7 mus musculu
65	4	10.3	29	11	Q8VHI0	Q8vhi0 mus musculu
66	4	10.3	29	11	Q9JLQ6	Q9jlq6 rattus norv
67	4	10.3	29	11	Q9WVC4	Q9wvc4 mus musculu
68	4	10.3	29	16	Q8CLI6	Q8cli6 yersinia pe
69	4	10.3	30	2	Q9R4Z7	Q9r4z7 neisseria c
70	4	10.3	30	2	Q9R5C4	Q9r5c4 comamonas.
71	4	10.3	30	2	Q9R4N4	Q9r4n4 staphylococ
72	4	10.3	30	2	O85590	O85590 chlamydia t
73	4	10.3	30	4	Q96EU1	Q96eu1 homo sapien
74	4	10.3	30	4	Q15980	Q15980 homo sapien
75	4	10.3	30	5	Q95P86	Q95p86 mesobuthus
76	4	10.3	30	6	Q8MHW1	Q8mhw1 sus scrofa
77	4	10.3	30	7	Q31234	Q31234 mus musculu
78	4	10.3	30	10	Q9S JL3	Q9sjl3 arabidopsis
79	4	10.3	30	11	Q9QV95	Q9qv95 cavia (guin
80	4	10.3	30	11	Q9QV42	Q9qv42 rattus sp.
81	4	10.3	30	12	P89878	P89878 molluscum c
82	4	10.3	30	16	Q8VJU1	Q8vj1 mycobacteri
83	4	10.3	30	16	Q8G2I8	Q8g2i8 brucella su
84	4	10.3	31	2	Q9S5Z5	Q9s5z5 streptomyce
85	4	10.3	31	2	Q9JP49	Q9jp49 azospirillu
86	4	10.3	31	2	Q9L7N7	Q9l7n7 borrelia af
87	4	10.3	31	2	Q9K WY1	Q9kwyl streptococc
88	4	10.3	31	4	Q9NYP6	Q9nyp6 homo sapien
89	4	10.3	31	6	O77625	O77625 bos taurus
90	4	10.3	31	6	Q95M83	Q95m83 equus cabal
91	4	10.3	31	10	Q9S8M6	Q9s8m6 lupinus alb
92	4	10.3	31	10	Q9FUQ2	Q9fuq2 zea mays (s
93	4	10.3	31	11	Q60419	Q60419 cricetus
94	4	10.3	31	13	Q91705	Q91705 xenopus lae
95	4	10.3	31	13	Q9W7F4	Q9w7f4 labeo rohit
96	4	10.3	31	16	Q9PGM7	Q9pgm7 xylella fas
97	4	10.3	31	16	Q8U5T3	Q8u5t3 agrobacteri
98	4	10.3	31	16	Q8VJ21	Q8vj21 mycobacteri
99	4	10.3	31	16	Q8VJ13	Q8vj13 mycobacteri
100	4	10.3	31	16	P74787	P74787 synechocyst
101	4	10.3	31	16	Q8NW38	Q8nw38 staphylococ
102	4	10.3	31	16	Q8E895	Q8e895 shewanella
103	4	10.3	32	2	Q44499	Q44499 anabaena va
104	4	10.3	32	3	P78708	P78708 neurospora
105	4	10.3	32	4	Q96RX4	Q96rx4 homo sapien
106	4	10.3	32	6	Q9BEF6	Q9bef6 capra hircu
107	4	10.3	32	8	Q8SL89	Q8sl89 euglena ste
108	4	10.3	32	8	Q9MS54	Q9ms54 euglena vir
109	4	10.3	32	10	Q9FUQ3	Q9fuq3 zea mays (s
110	4	10.3	32	10	Q9FE82	Q9fe82 zea mays (s
111	4	10.3	32	10	Q9FE81	Q9fe81 zea mays (s
112	4	10.3	32	10	Q9FUQ1	Q9fuq1 zea mays (s
113	4	10.3	32	10	Q9FUQ5	Q9fuq5 zea mays su
114	4	10.3	32	10	Q9FUP9	Q9fup9 zea luxuria

115	4	10.3	32	10	Q9FUQ4	Q9fuq4 zea mays (s
116	4	10.3	32	10	Q9FUQ0	Q9fug0 zea luxuria
117	4	10.3	32	10	Q9FE80	Q9fe80 zea diplope
118	4	10.3	32	10	Q9FUP8	Q9fup8 zea luxuria
119	4	10.3	32	11	Q9JIU1	Q9jiu1 rattus norv
120	4	10.3	32	11	Q9R1C2	Q9rlc2 mus musculu
121	4	10.3	32	13	Q57364	Q57364 brachydanio
122	4	10.3	32	13	Q9YGR4	Q9ygr4 gallus gall
123	4	10.3	32	16	Q932N6	Q932n6 staphylococ
124	4	10.3	32	16	Q8VJ76	Q8vj76 mycobacteri
125	4	10.3	32	16	Q9K4G0	Q9k4g0 streptomyce
126	4	10.3	32	16	Q8EJG9	Q8ejg9 shewanella
127	4	10.3	32	16	Q8EBJ9	Q8ebj9 shewanella
128	4	10.3	32	17	Q9HNL3	Q9hn13 halobacteri
129	4	10.3	33	2	O30547	O30547 pseudomonas
130	4	10.3	33	2	Q45283	Q45283 bacillus li
131	4	10.3	33	4	Q8IZ90	Q8iz90 homo sapien
132	4	10.3	33	8	Q9MS60	Q9ms60 euglena san
133	4	10.3	33	8	Q9MS57	Q9ms57 euglena ste
134	4	10.3	33	8	Q8HUN2	Q8hun2 populus tom
135	4	10.3	33	12	O11372	O11372 molluscum c
136	4	10.3	33	13	Q9PS28	Q9ps28 cerastes ce
137	4	10.3	33	16	Q9KTZ5	Q9ktz5 vibrio chol
138	4	10.3	33	16	Q97RJ3	Q97rj3 streptococc
139	4	10.3	33	16	Q932N2	Q932n2 staphylococ
140	4	10.3	33	16	Q8U5P2	Q8u5p2 agrobacteri
141	4	10.3	33	16	Q8VJZ2	Q8vjz2 mycobacteri
142	4	10.3	33	16	Q8P8K6	Q8p8k6 xanthomonas
143	4	10.3	33	16	Q8G114	Q8g114 brucella su
144	4	10.3	33	16	Q8FY86	Q8fy86 brucella su
145	4	10.3	33	16	Q8EBD6	Q8ebd6 shewanella
146	4	10.3	33	16	Q8CQY7	Q8cqy7 staphylococ
147	4	10.3	33	16	Q8CLN5	Q8cln5 yersinia pe
148	4	10.3	33	17	Q8ZY37	Q8zy37 pyrobaculum
149	4	10.3	34	2	Q9Z4Q3	Q9z4q3 corynebacte
150	4	10.3	34	2	Q9S3W3	Q9s3w3 mastigoclad
151	4	10.3	34	2	Q9RE23	Q9re23 helicobacte
152	4	10.3	34	4	Q9UI64	Q9ui64 homo sapien
153	4	10.3	34	4	Q96IX0	Q96ix0 homo sapien
154	4	10.3	34	4	Q96J93	Q96j93 homo sapien
155	4	10.3	34	5	Q8T3M2	Q8t3m2 drosophila
156	4	10.3	34	8	Q9GI95	Q9gi95 sargassum s
157	4	10.3	34	8	Q32752	Q32752 oryza sativ
158	4	10.3	34	11	Q925F8	Q925f8 rattus norv
159	4	10.3	34	11	Q8VHL4	Q8vh14 rattus norv
160	4	10.3	34	12	Q9E8K5	Q9e8k5 hepatitis b
161	4	10.3	34	16	Q8EHU5	Q8ehu5 shewanella
162	4	10.3	34	16	Q8CLQ6	Q8clq6 yersinia pe
163	4	10.3	34	17	Q9HMS8	Q9hms8 halobacteri
164	4	10.3	35	2	Q9RE20	Q9re20 helicobacte
165	4	10.3	35	2	Q9RE26	Q9re26 helicobacte
166	4	10.3	35	2	Q53272	Q53272 escherichia
167	4	10.3	35	2	Q9RE21	Q9re21 helicobacte
168	4	10.3	35	2	Q9R2Y4	Q9r2y4 helicobacte
169	4	10.3	35	2	Q9RE27	Q9re27 helicobacte
170	4	10.3	35	2	Q51963	Q51963 pseudomonas
171	4	10.3	35	2	O53109	O53109 mycoplasma

172	4	10.3	35	2	Q8KM41	Q8km41 mycobacteri
173	4	10.3	35	2	Q9RE24	Q9re24 helicobacte
174	4	10.3	35	2	Q9RE25	Q9re25 helicobacte
175	4	10.3	35	2	Q9R2Y5	Q9r2y5 helicobacte
176	4	10.3	35	2	Q8VT19	Q8vt19 enterococcu
177	4	10.3	35	2	Q9R2Y6	Q9r2y6 helicobacte
178	4	10.3	35	2	Q9RE22	Q9re22 helicobacte
179	4	10.3	35	3	O14374	O14374 schizosacch
180	4	10.3	35	4	Q96RX9	Q96rx9 homo sapien
181	4	10.3	35	4	Q9UED0	Q9ued0 homo sapien
182	4	10.3	35	5	Q9GTB7	Q9gtb7 neospora ca
183	4	10.3	35	10	Q8GUX3	Q8gux3 picea maria
184	4	10.3	35	13	Q09133	Q09133 xenopus lae
185	4	10.3	35	15	Q8UT29	Q8ut29 human immun
186	4	10.3	35	16	Q9PPG6	Q9ppg6 campylobact
187	4	10.3	35	16	Q8Z0F9	Q8z0f9 anabaena sp
188	4	10.3	35	16	Q8U5A2	Q8u5a2 agrobacteri
189	4	10.3	35	16	Q8VKN5	Q8vkn5 mycobacteri
190	4	10.3	36	2	O53108	O53108 mycoplasma
191	4	10.3	36	2	Q44153	Q44153 actinobacil
192	4	10.3	36	4	Q96G89	Q96g89 homo sapien
193	4	10.3	36	4	Q9UI80	Q9ui80 homo sapien
194	4	10.3	36	6	Q8SPM7	Q8spm7 canis famil
195	4	10.3	36	8	O79185	O79185 ninox rufa.
196	4	10.3	36	10	Q8W502	Q8w502 dichelostem
197	4	10.3	36	11	Q920Z5	Q920z5 rattus sp.
198	4	10.3	36	16	O50686	O50686 borrelia bu
199	4	10.3	36	16	Q9A5R6	Q9a5r6 caulobacter
200	4	10.3	36	16	Q8PK38	Q8pk38 xanthomonas
201	4	10.3	36	16	Q8EYJ2	Q8eyj2 leptospira
202	4	10.3	36	16	Q8EC61	Q8ec61 shewanella
203	4	10.3	36	16	Q8EBV5	Q8ebv5 shewanella
204	4	10.3	37	4	Q9BW21	Q9bw21 homo sapien
205	4	10.3	37	4	Q8TD81	Q8td81 homo sapien
206	4	10.3	37	4	Q96HV0	Q96hv0 homo sapien
207	4	10.3	37	5	Q17245	Q17245 bombyx mori
208	4	10.3	37	5	Q17244	Q17244 bombyx mori
209	4	10.3	37	5	Q8MPH4	Q8mph4 schistosoma
210	4	10.3	37	9	Q8HAH3	Q8hah3 salmonella
211	4	10.3	37	10	Q9S8D8	Q9s8d8 malus domes
212	4	10.3	37	11	Q8BMY3	Q8bmy3 mus musculu
213	4	10.3	37	12	Q98151	Q98151 kaposi's sa
214	4	10.3	37	12	Q8AYZ0	Q8ayz0 goose circo
215	4	10.3	37	12	Q8AYY4	Q8ayy4 goose circo
216	4	10.3	37	13	Q9PRK6	Q9prk6 gallus sp.
217	4	10.3	37	13	O57376	O57376 brachydanio
218	4	10.3	37	13	Q9PRK1	Q9prk1 gallus sp.
219	4	10.3	37	16	Q9X089	Q9x089 thermotoga
220	4	10.3	37	16	Q9KPZ4	Q9kpz4 vibrio chol
221	4	10.3	37	16	Q9KEJ6	Q9kej6 bacillus ha
222	4	10.3	37	16	Q8KD28	Q8kd28 chlorobium
223	4	10.3	37	16	Q8FVV0	Q8fvv0 brucella su
224	4	10.3	37	16	Q8EIQ2	Q8eiq2 shewanella
225	4	10.3	37	17	Q9HRW1	Q9hrw1 halobacteri
226	4	10.3	38	2	Q9F5C7	Q9f5c7 agrobacteri
227	4	10.3	38	2	Q9R7M2	Q9r7m2 escherichia
228	4	10.3	38	2	Q8KYC9	Q8kyc9 bacillus an

229	4	10.3	38	2	Q939W1	Q939w1 aeromonas s
230	4	10.3	38	2	Q8GN7	Q8gnn7 escherichia
231	4	10.3	38	4	Q8TDB1	Q8tdb1 homo sapien
232	4	10.3	38	4	Q8IZ88	Q8iz88 homo sapien
233	4	10.3	38	5	Q96617	Q96617 echinococcu
234	4	10.3	38	11	Q91XM1	Q91xml1 rattus norv
235	4	10.3	38	13	Q9PTV6	Q9ptv6 oryzias lat
236	4	10.3	38	13	Q9PTV7	Q9ptv7 oryzias lat
237	4	10.3	38	15	Q55472	Q55472 human immun
238	4	10.3	38	16	Q9KLC0	Q9klc0 vibrio chol
239	4	10.3	38	17	Q8ZX52	Q8zx52 pyrobaculum
240	4	10.3	39	4	Q9NQQ8	Q9nqq8 homo sapien
241	4	10.3	39	4	Q9UD56	Q9ud56 homo sapien
242	4	10.3	39	4	Q9UD60	Q9ud60 homo sapien
243	4	10.3	39	4	Q9UC03	Q9uc03 homo sapien
244	4	10.3	39	5	Q23904	Q23904 dictyosteli
245	4	10.3	39	5	Q9V8G0	Q9v8g0 drosophila
246	4	10.3	39	8	Q9XLU0	Q9xlu0 saccharomyc
247	4	10.3	39	8	Q36197	Q36197 ursus arcto
248	4	10.3	39	12	Q9IW57	Q9iw57 borna disea
249	4	10.3	39	13	Q73604	Q73604 gallus gall
250	4	10.3	39	16	Q9PFD3	Q9pdf3 xylella fas
251	4	10.3	39	16	Q9KM79	Q9km79 vibrio chol
252	4	10.3	39	16	Q9A7N6	Q9a7n6 caulobacter
253	4	10.3	39	16	Q8ZK28	Q8zk28 salmonella
254	4	10.3	39	16	Q8X406	Q8x406 escherichia
255	4	10.3	39	16	Q8VK19	Q8vk19 mycobacteri
256	4	10.3	39	16	Q9KXN7	Q9kxn7 streptomyce
257	4	10.3	39	16	Q8DXQ2	Q8dxq2 streptococc
258	4	10.3	40	2	Q55331	Q55331 synechocyst
259	4	10.3	40	2	Q69584	Q69584 mycobacteri
260	4	10.3	40	3	Q9URF6	Q9urf6 saccharomyc
261	4	10.3	40	4	Q8WYE5	Q8wye5 homo sapien
262	4	10.3	40	5	Q9UAF4	Q9uaf4 halocynthia
263	4	10.3	40	5	Q8IME0	Q8ime0 drosophila
264	4	10.3	40	7	Q9TNZ4	Q9tnz4 rattus norv
265	4	10.3	40	8	Q05333	Q05333 petunia sp.
266	4	10.3	40	8	Q8MFP6	Q8mfp6 vitis vinif
267	4	10.3	40	10	Q8S5P4	Q8s5p4 oryza sativ
268	4	10.3	40	11	Q923H1	Q923h1 cricetus
269	4	10.3	40	13	Q9PRT5	Q9prt5 rana catesbe
270	4	10.3	40	16	Q24910	Q24910 helicobacte
271	4	10.3	40	16	Q9I1X6	Q9i1x6 pseudomonas
272	4	10.3	40	16	Q935Q4	Q935q4 salmonella
273	4	10.3	40	16	Q8KE46	Q8ke46 chlorobium
274	4	10.3	40	16	Q8EYM7	Q8eym7 leptospira
275	4	10.3	40	16	Q8EXS6	Q8exs6 leptospira
276	4	10.3	40	16	Q8EGK3	Q8egk3 shewanella
277	3	7.7	28	1	Q9UWI5	Q9uwi5 archaeoglob
278	3	7.7	28	1	Q9UWL1	Q9uw1 pyrococcus
279	3	7.7	28	2	Q47565	Q47565 escherichia
280	3	7.7	28	2	Q47354	Q47354 escherichia
281	3	7.7	28	2	Q47372	Q47372 escherichia
282	3	7.7	28	2	Q47373	Q47373 escherichia
283	3	7.7	28	2	Q9R4Z1	Q9r4z1 chloroflexu
284	3	7.7	28	2	Q47368	Q47368 escherichia
285	3	7.7	28	2	Q47359	Q47359 escherichia

286	3	7.7	28	2	Q47371	Q47371 escherichia
287	3	7.7	28	2	Q47358	Q47358 escherichia
288	3	7.7	28	2	Q9R5I4	Q9r5i4 streptococc
289	3	7.7	28	2	Q47365	Q47365 escherichia
290	3	7.7	28	2	Q47370	Q47370 escherichia
291	3	7.7	28	2	Q9R4G6	Q9r4g6 eubacterium
292	3	7.7	28	2	Q52275	Q52275 pseudomonas
293	3	7.7	28	2	Q9F7C1	Q9f7c1 serratia ma
294	3	7.7	28	2	Q47352	Q47352 escherichia
295	3	7.7	28	2	Q47736	Q47736 enterococcu
296	3	7.7	28	2	Q47357	Q47357 escherichia
297	3	7.7	28	2	Q49327	Q49327 mycoplasma
298	3	7.7	28	2	Q9R5E6	Q9r5e6 thermus aqu
299	3	7.7	28	2	Q47369	Q47369 escherichia
300	3	7.7	28	2	Q9REI4	Q9rei4 acidiphiliu
301	3	7.7	28	2	Q9R4L5	Q9r4l5 helicobacte
302	3	7.7	28	2	Q47360	Q47360 escherichia
303	3	7.7	28	2	Q47366	Q47366 escherichia
304	3	7.7	28	2	Q52623	Q52623 proteus vul
305	3	7.7	28	2	Q47367	Q47367 escherichia
306	3	7.7	28	2	Q46752	Q46752 escherichia
307	3	7.7	28	2	Q9R5C7	Q9r5c7 vibrio para
308	3	7.7	28	2	Q08005	Q08005 lactococcus
309	3	7.7	28	2	Q47356	Q47356 escherichia
310	3	7.7	28	2	Q93JY6	Q93jy6 mycobacteri
311	3	7.7	28	2	Q47363	Q47363 escherichia
312	3	7.7	28	2	Q93KE4	Q93ke4 chlamydia p
313	3	7.7	28	2	Q9R4X0	Q9r4x0 synechococc
314	3	7.7	28	2	Q9ZB83	Q9zb83 vibrio angu
315	3	7.7	28	3	P87021	P87021 magnaporthe
316	3	7.7	28	3	Q00440	Q00440 glomerella
317	3	7.7	28	4	Q8N670	Q8n670 homo sapien
318	3	7.7	28	4	Q8N2V3	Q8n2v3 homo sapien
319	3	7.7	28	4	O43804	O43804 homo sapien
320	3	7.7	28	4	Q9UD92	Q9ud92 homo sapien
321	3	7.7	28	4	Q9H4R8	Q9h4r8 homo sapien
322	3	7.7	28	4	Q8WUY6	Q8wuy6 homo sapien
323	3	7.7	28	4	Q8NG21	Q8ng21 homo sapien
324	3	7.7	28	4	Q16325	Q16325 homo sapien
325	3	7.7	28	4	Q9UMB1	Q9umb1 homo sapien
326	3	7.7	28	4	Q15839	Q15839 homo sapien
327	3	7.7	28	4	Q9HB33	Q9hb33 homo sapien
328	3	7.7	28	4	Q9NQR3	Q9nqr3 homo sapien
329	3	7.7	28	4	Q8J018	Q8j018 homo sapien
330	3	7.7	28	4	Q8IZT7	Q8izt7 homo sapien
331	3	7.7	28	4	Q8IZL0	Q8izl0 homo sapien
332	3	7.7	28	4	Q8IZK3	Q8izk3 homo sapien
333	3	7.7	28	4	Q8IZK2	Q8izk2 homo sapien
334	3	7.7	28	4	Q8IZ87	Q8iz87 homo sapien
335	3	7.7	28	5	Q9BM57	Q9bm57 lineus sp.
336	3	7.7	28	5	Q9BM76	Q9bm76 giardia lam
337	3	7.7	28	5	Q9BM74	Q9bm74 giardia lam
338	3	7.7	28	5	Q9TWT9	Q9twt9 penaeus jap
339	3	7.7	28	5	Q95NM7	Q95nm7 lithobius f
340	3	7.7	28	5	Q9GPK8	Q9gpk8 scutigerell
341	3	7.7	28	5	Q9BM75	Q9bm75 giardia lam
342	3	7.7	28	6	Q9TRM4	Q9trm4 bos taurus

343	3	7.7	28	6	Q62731	062731 canis famil
344	3	7.7	28	6	Q9TRV2	Q9trv2 canis famil
345	3	7.7	28	6	Q9XS67	Q9xs67 bos taurus
346	3	7.7	28	6	Q9TU57	Q9tu57 papio cynoc
347	3	7.7	28	6	Q62821	062821 bubalus bub
348	3	7.7	28	6	Q9TU56	Q9tu56 colobus gue
349	3	7.7	28	6	Q9TU58	Q9tu58 trachypithe
350	3	7.7	28	6	Q8WP02	Q8wp02 ateles belz
351	3	7.7	28	7	O19736	O19736 homo sapien
352	3	7.7	28	7	O19732	O19732 homo sapien
353	3	7.7	28	8	Q8WK64	Q8wk64 pinus leiop
354	3	7.7	28	8	Q8WK92	Q8wk92 pinus carib
355	3	7.7	28	8	Q8WK52	Q8wk52 pinus herre
356	3	7.7	28	8	Q8WK78	Q8wk78 pinus palus
357	3	7.7	28	8	Q8WK60	Q8wk60 pinus oocar
358	3	7.7	28	8	Q8WK44	Q8wk44 pinus roxbu
359	3	7.7	28	8	Q8WK48	Q8wk48 pinus dougl
360	3	7.7	28	8	Q8WK94	Q8wk94 pinus atten
361	3	7.7	28	8	Q8WK66	Q8wk66 pinus virgi
362	3	7.7	28	8	Q8WK74	Q8wk74 pinus punge
363	3	7.7	28	8	Q8WK70	Q8wk70 pinus taeda
364	3	7.7	28	8	Q8WK54	Q8wk54 pinus carib
365	3	7.7	28	8	Q9ZYV5	Q9zyv5 dipsosaurus
366	3	7.7	28	8	Q9T2U2	Q9t2u2 bos taurus
367	3	7.7	28	8	Q33554	Q33554 crithidia f
368	3	7.7	28	8	Q8WK50	Q8wk50 pinus muric
369	3	7.7	28	8	Q37005	Q37005 oryza sativ
370	3	7.7	28	8	Q8WK72	Q8wk72 pinus rigid
371	3	7.7	28	8	Q9G5Y8	Q9g5y8 agama agama
372	3	7.7	28	8	Q8WK86	Q8wk86 pinus conto
373	3	7.7	28	8	Q8WK62	Q8wk62 pinus patul
374	3	7.7	28	8	Q8WK84	Q8wk84 pinus cuben
375	3	7.7	28	8	Q8WK88	Q8wk88 pinus carib
376	3	7.7	28	8	Q8WK82	Q8wk82 pinus maest
377	3	7.7	28	8	Q8WK58	Q8wk58 pinus radia
378	3	7.7	28	8	Q8WK80	Q8wk80 pinus mugo.
379	3	7.7	28	8	Q8WK56	Q8wk56 pinus resin
380	3	7.7	28	8	Q8WK90	Q8wk90 pinus banks
381	3	7.7	28	8	Q8LVZ6	Q8lvz6 astyanax al
382	3	7.7	28	8	Q8WK76	Q8wk76 pinus ponde
383	3	7.7	28	8	Q8MAY2	Q8may2 porana pani
384	3	7.7	28	8	Q8WK68	Q8wk68 pinus tropi
385	3	7.7	28	8	Q8HS23	Q8hs23 pisum sativ
386	3	7.7	28	8	Q8HS11	Q8hs11 spathiphyll
387	3	7.7	28	8	Q8HS07	Q8hs07 welwitschia
388	3	7.7	28	8	Q8HQU4	Q8hqu4 pinus jeffr
389	3	7.7	28	8	Q8HQU2	Q8hqu2 pinus engel
390	3	7.7	28	8	Q8HQR7	Q8hqr7 pinus ellio
391	3	7.7	28	8	Q8HQR5	Q8hqr5 pinus serot
392	3	7.7	28	8	Q8HQR3	Q8hqr3 pinus echin
393	3	7.7	28	10	Q8S6H4	Q8s6h4 oryza sativ
394	3	7.7	28	10	Q9XGH2	Q9xgh2 pisum sativ
395	3	7.7	28	10	Q9SAR3	Q9sar3 solanum tub
396	3	7.7	28	10	Q9XGE3	Q9xge3 vicia faba
397	3	7.7	28	10	O24218	O24218 oryza sativ
398	3	7.7	28	10	Q9XGE4	Q9xge4 vicia faba
399	3	7.7	28	10	Q41098	Q41098 populus bal

400	3	7.7	28	11	Q99PC4	Q99pc4 mus musculu
401	3	7.7	28	11	Q91XP0	Q91xp0 rattus norv
402	3	7.7	28	11	Q9EQ26	Q9eq26 mus musculu
403	3	7.7	28	11	Q91VP0	Q91vp0 mus musculu
404	3	7.7	28	12	Q67747	Q67747 human adeno
405	3	7.7	28	12	Q67782	Q67782 human adeno
406	3	7.7	28	12	Q67778	Q67778 human adeno
407	3	7.7	28	12	Q67781	Q67781 human adeno
408	3	7.7	28	12	Q67787	Q67787 human adeno
409	3	7.7	28	12	Q67754	Q67754 human adeno
410	3	7.7	28	12	Q67780	Q67780 human adeno
411	3	7.7	28	12	Q67756	Q67756 human adeno
412	3	7.7	28	12	Q67777	Q67777 human adeno
413	3	7.7	28	12	Q9QC16	Q9qc16 hepatitis c
414	3	7.7	28	12	Q67773	Q67773 human adeno
415	3	7.7	28	12	Q67769	Q67769 human adeno
416	3	7.7	28	12	Q67767	Q67767 human adeno
417	3	7.7	28	12	Q67761	Q67761 human adeno
418	3	7.7	28	12	Q67783	Q67783 human adeno
419	3	7.7	28	12	Q67757	Q67757 human adeno
420	3	7.7	28	12	Q9QC46	Q9qc46 hepatitis c
421	3	7.7	28	12	Q67764	Q67764 human adeno
422	3	7.7	28	12	Q9QC19	Q9qc19 hepatitis c
423	3	7.7	28	12	Q67755	Q67755 human adeno
424	3	7.7	28	12	Q67762	Q67762 human adeno
425	3	7.7	28	12	Q67784	Q67784 human adeno
426	3	7.7	28	12	Q67763	Q67763 human adeno
427	3	7.7	28	12	Q9QC14	Q9qc14 hepatitis c
428	3	7.7	28	12	Q67772	Q67772 human adeno
429	3	7.7	28	12	Q98130	Q98130 kaposi's sa
430	3	7.7	28	12	Q9QC24	Q9qc24 hepatitis c
431	3	7.7	28	12	Q67765	Q67765 human adeno
432	3	7.7	28	12	Q67766	Q67766 human adeno
433	3	7.7	28	12	Q67776	Q67776 human adeno
434	3	7.7	28	12	Q67775	Q67775 human adeno
435	3	7.7	28	12	Q9QC17	Q9qc17 hepatitis c
436	3	7.7	28	12	Q67774	Q67774 human adeno
437	3	7.7	28	12	Q67745	Q67745 human adeno
438	3	7.7	28	12	Q67758	Q67758 human adeno
439	3	7.7	28	12	Q67760	Q67760 human adeno
440	3	7.7	28	12	Q67771	Q67771 human adeno
441	3	7.7	28	12	Q83181	Q83181 cauliflower
442	3	7.7	28	12	Q67752	Q67752 human adeno
443	3	7.7	28	12	Q68009	Q68009 hepatitis b
444	3	7.7	28	12	Q68552	Q68552 hepatitis c
445	3	7.7	28	12	Q67753	Q67753 human adeno
446	3	7.7	28	12	Q67751	Q67751 human adeno
447	3	7.7	28	12	Q67770	Q67770 human adeno
448	3	7.7	28	12	Q67779	Q67779 human adeno
449	3	7.7	28	12	Q67750	Q67750 human adeno
450	3	7.7	28	12	Q67748	Q67748 human adeno
451	3	7.7	28	12	Q67768	Q67768 human adeno
452	3	7.7	28	12	Q9QC18	Q9qc18 hepatitis c
453	3	7.7	28	12	Q86649	Q86649 murine hepa
454	3	7.7	28	12	Q67785	Q67785 human adeno
455	3	7.7	28	12	Q9QC35	Q9qc35 hepatitis c
456	3	7.7	28	12	Q67746	Q67746 human adeno

457	3	7.7	28	12	Q67749	Q67749 human adeno
458	3	7.7	28	12	Q67759	Q67759 human adeno
459	3	7.7	28	13	Q9DD70	Q9dd70 gallus gall
460	3	7.7	28	13	Q90757	Q90757 gallus gall
461	3	7.7	28	13	Q9PRN9	Q9prn9 carassius a
462	3	7.7	28	13	Q9YH39	Q9yh39 xiphophorus
463	3	7.7	28	13	Q9PRI9	Q9pri9 amia calva
464	3	7.7	28	13	Q9PRN8	Q9prn8 carassius a
465	3	7.7	28	13	Q90W61	Q90w61 xenopus lae
466	3	7.7	28	13	Q9PRX4	Q9prx4 xenopus lae
467	3	7.7	28	13	Q8QFT6	Q8qft6 gallus gall
468	3	7.7	28	15	O71346	O71346 human endog
469	3	7.7	28	15	P89161	P89161 chimpanzee
470	3	7.7	28	15	Q72263	Q72263 human immun
471	3	7.7	28	16	Q9KDN3	Q9kdn3 bacillus ha
472	3	7.7	28	16	Q9KDN2	Q9kdn2 bacillus ha
473	3	7.7	28	16	Q9K9U0	Q9k9u0 bacillus ha
474	3	7.7	28	16	Q8Y051	Q8y051 ralstonia s
475	3	7.7	28	16	Q8X415	Q8x415 escherichia
476	3	7.7	28	16	Q8PB05	Q8pb05 xanthomonas
477	3	7.7	28	16	Q8E014	Q8e014 streptococc
478	3	7.7	28	16	Q8CLV6	Q8clv6 yersinia pe
479	3	7.7	28	16	Q8CKG3	Q8ckg3 yersinia pe
480	3	7.7	29	2	Q9ZG52	Q9zg52 chlamydia t
481	3	7.7	29	2	Q54200	Q54200 streptomyce
482	3	7.7	29	2	Q9L928	Q91928 shigella so
483	3	7.7	29	2	Q9X3E3	Q9x3e3 prochloroco
484	3	7.7	29	2	Q9S3J5	Q9s3j5 escherichia
485	3	7.7	29	2	Q47633	Q47633 escherichia
486	3	7.7	29	2	Q9L926	Q9l926 shigella fl
487	3	7.7	29	2	Q9AKV1	Q9akv1 neisseria g
488	3	7.7	29	2	Q9R9K0	Q9r9k0 paracoccus
489	3	7.7	29	2	Q9R511	Q9r511 bacillus su
490	3	7.7	29	2	Q59396	Q59396 escherichia
491	3	7.7	29	2	Q938P6	Q938p6 borrelia bu
492	3	7.7	29	2	Q9R4B7	Q9r4b7 streptomyce
493	3	7.7	29	2	Q9L924	Q9l924 shigella bo
494	3	7.7	29	2	Q9F7A0	Q9f7a0 salmonella
495	3	7.7	29	2	Q9R5G9	Q9r5g9 rhodococcus
496	3	7.7	29	2	Q51692	Q51692 paracoccus
497	3	7.7	29	2	Q47389	Q47389 escherichia
498	3	7.7	29	2	Q8VV94	Q8vv94 marine psyc
499	3	7.7	29	2	Q9R5M6	Q9r5m6 streptomyce
500	3	7.7	29	3	Q9HDQ2	Q9hdq2 candida rug
501	3	7.7	29	3	P78747	P78747 saccharomyc
502	3	7.7	29	3	Q9UR77	Q9ur77 candida alb
503	3	7.7	29	4	Q8WVE2	Q8wve2 homo sapien
504	3	7.7	29	4	Q9UM98	Q9um98 homo sapien
505	3	7.7	29	4	Q9P2A1	Q9p2a1 homo sapien
506	3	7.7	29	4	Q9UCR6	Q9ucr6 homo sapien
507	3	7.7	29	4	Q9UM88	Q9um88 homo sapien
508	3	7.7	29	4	Q9UGJ6	Q9ugj6 homo sapien
509	3	7.7	29	4	Q8N2Z7	Q8n2z7 homo sapien
510	3	7.7	29	4	Q9UKX9	Q9ukx9 homo sapien
511	3	7.7	29	4	Q9UN87	Q9un87 homo sapien
512	3	7.7	29	4	Q8NEF6	Q8nef6 homo sapien
513	3	7.7	29	4	O43807	O43807 homo sapien

514	3	7.7	29	4	Q9UCL2	Q9uc12	homo sapien
515	3	7.7	29	4	Q96FP2	Q96fp2	homo sapien
516	3	7.7	29	4	Q9BX18	Q9bx18	homo sapien
517	3	7.7	29	4	Q9BV72	Q9bv72	homo sapien
518	3	7.7	29	4	Q9Y447	Q9y447	homo sapien
519	3	7.7	29	4	Q9BYJ8	Q9byj8	homo sapien
520	3	7.7	29	5	Q9TWN8	Q9twn8	pseudaleitia
521	3	7.7	29	5	Q8T3E8	Q8t3e8	caenorhabdi
522	3	7.7	29	5	Q9TWS4	Q9tws4	hirudinaria
523	3	7.7	29	5	Q26819	Q26819	trypanosoma
524	3	7.7	29	5	Q17073	Q17073	antheraea p
525	3	7.7	29	5	Q967U4	Q967u4	schistocerc
526	3	7.7	29	5	Q9GU41	Q9gu41	sycon rapha
527	3	7.7	29	5	Q95SA8	Q95sa8	drosophila
528	3	7.7	29	5	Q967U5	Q967u5	schistocerc
529	3	7.7	29	5	Q27301	Q27301	drosophila
530	3	7.7	29	5	Q8ITD6	Q8itd6	schistosoma
531	3	7.7	29	6	Q9TSS7	Q9tss7	felis silve
532	3	7.7	29	6	Q8WP11	Q8wp11	ateles belz
533	3	7.7	29	6	Q95LA5	Q95la5	macaca mula
534	3	7.7	29	6	Q9TU60	Q9tu60	gorilla gor
535	3	7.7	29	6	Q9MZW8	Q9mzw8	pongo pygma
536	3	7.7	29	6	Q9TU63	Q9tu63	pan paniscu
537	3	7.7	29	6	Q9TU62	Q9tu62	pan troglod
538	3	7.7	29	6	Q9N1W3	Q9n1w3	equus cabal
539	3	7.7	29	6	Q9TS04	Q9ts04	bos taurus
540	3	7.7	29	7	Q9TPN3	Q9tpn3	agelaius ph
541	3	7.7	29	7	Q9TPN0	Q9tpn0	agelaius ph
542	3	7.7	29	7	Q9XRK6	Q9xrk6	agelaius ph
543	3	7.7	29	7	Q9TPM5	Q9tpm5	agelaius ph
544	3	7.7	29	7	Q9XRK7	Q9xrk7	agelaius ph
545	3	7.7	29	7	Q9TPN6	Q9tpn6	agelaius ph
546	3	7.7	29	7	Q9TPM9	Q9tpm9	agelaius ph
547	3	7.7	29	7	Q9TPN5	Q9tpn5	agelaius ph
548	3	7.7	29	7	Q9TPM6	Q9tpm6	agelaius ph
549	3	7.7	29	7	Q9TPN2	Q9tpn2	agelaius ph
550	3	7.7	29	7	Q9XRK5	Q9xrk5	agelaius ph
551	3	7.7	29	7	Q9TPN1	Q9tpn1	agelaius ph
552	3	7.7	29	7	Q9XRD9	Q9xrd9	agelaius ph
553	3	7.7	29	7	Q30139	Q30139	homo sapien
554	3	7.7	29	7	Q9XRK3	Q9xrk3	agelaius ph
555	3	7.7	29	7	Q9TPN8	Q9tpn8	agelaius ph
556	3	7.7	29	7	Q9TPM7	Q9tpm7	agelaius ph
557	3	7.7	29	7	Q9TPP0	Q9tpp0	agelaius ph
558	3	7.7	29	7	Q9TPK6	Q9tpk6	agelaius ph
559	3	7.7	29	7	Q9TPN7	Q9tpn7	agelaius ph
560	3	7.7	29	7	Q9XRK4	Q9xrk4	agelaius ph
561	3	7.7	29	7	Q9TPM8	Q9tpm8	agelaius ph
562	3	7.7	29	7	Q9TPN4	Q9tpn4	agelaius ph
563	3	7.7	29	7	Q9TPN9	Q9tpn9	agelaius ph
564	3	7.7	29	7	Q06653	Q06653	homo sapien
565	3	7.7	29	8	Q9G5Z1	Q9g5z1	pseudocalot
566	3	7.7	29	8	Q9G657	Q9g657	japalura tr
567	3	7.7	29	8	Q9GF70	Q9gf70	trochodendr
568	3	7.7	29	8	Q9G615	Q9g615	cophotis ce
569	3	7.7	29	8	Q33131	Q33131	spinacia ol
570	3	7.7	29	8	Q9TI61	Q9ti61	allosyncarp

571	3	7.7	29	8	Q9G648	Q9g648 sitana pont
572	3	7.7	29	8	Q9G370	Q9g370 draco blanf
573	3	7.7	29	8	Q9G352	Q9g352 laudakia sa
574	3	7.7	29	8	O03087	O03087 anthoceros
575	3	7.7	29	8	Q8WD25	Q8wd25 ctenophorus
576	3	7.7	29	8	O03120	O03120 megaceros v
577	3	7.7	29	8	Q8HS21	Q8hs21 rheum x cul
578	3	7.7	29	9	Q9ZX23	Q9zx23 mycobacteri
579	3	7.7	29	10	Q9FUR9	Q9fur9 physcomitre
580	3	7.7	29	10	Q8RUM7	Q8rum7 zea mays (m
581	3	7.7	29	10	Q94JL6	Q94jl6 hevea brasi
582	3	7.7	29	10	Q42243	Q42243 arabidopsis
583	3	7.7	29	10	Q08065	Q08065 zea mays (m
584	3	7.7	29	10	Q8H772	Q8h772 arabidopsis
585	3	7.7	29	11	Q9CSI4	Q9csi4 mus musculu
586	3	7.7	29	11	Q9QVB1	Q9qvb1 rattus sp.
587	3	7.7	29	11	Q921Z6	Q921z6 mus musculu
588	3	7.7	29	11	Q64353	Q64353 mus musculu
589	3	7.7	29	11	O88214	O88214 mus musculu
590	3	7.7	29	11	Q8VIF4	Q8vif4 mus musculu
591	3	7.7	29	11	Q62777	Q62777 rattus norv
592	3	7.7	29	11	Q99JY5	Q99jy5 mus musculu
593	3	7.7	29	11	O88213	O88213 mus musculu
594	3	7.7	29	11	Q9QY65	Q9qy65 mus musculu
595	3	7.7	29	11	Q8R398	Q8r398 mus musculu
596	3	7.7	29	11	Q62300	Q62300 mus musculu
597	3	7.7	29	11	O08980	O08980 mus musculu
598	3	7.7	29	11	Q8CJ37	Q8cj37 mus musculu
599	3	7.7	29	12	Q91HB1	Q91hb1 porcine cir
600	3	7.7	29	12	O92646	O92646 hepatitis e
601	3	7.7	29	12	Q9DH48	Q9dh48 bovine coro
602	3	7.7	29	12	Q86872	Q86872 cauliflower
603	3	7.7	29	12	O92648	O92648 hepatitis e
604	3	7.7	29	12	O56835	O56835 vibrio chol
605	3	7.7	29	12	Q9QAR4	Q9qar4 bovine coro
606	3	7.7	29	13	O42547	O42547 brachydanio
607	3	7.7	29	13	P82234	P82234 rana tempor
608	3	7.7	29	13	Q8AYR0	Q8ayr0 oryzias lat
609	3	7.7	29	15	O72001	O72001 human endog
610	3	7.7	29	15	O71342	O71342 human endog
611	3	7.7	29	15	O71339	O71339 human endog
612	3	7.7	29	15	O71347	O71347 human endog
613	3	7.7	29	15	O71340	O71340 human endog
614	3	7.7	29	15	O71343	O71343 human endog
615	3	7.7	29	15	Q69897	Q69897 human immun
616	3	7.7	29	15	O71991	O71991 human endog
617	3	7.7	29	15	O71994	O71994 human endog
618	3	7.7	29	15	O71341	O71341 human endog
619	3	7.7	29	15	O71345	O71345 human endog
620	3	7.7	29	15	O71336	O71336 human endog
621	3	7.7	29	15	O71344	O71344 human endog
622	3	7.7	29	15	O71338	O71338 human endog
623	3	7.7	29	15	O71992	O71992 human endog
624	3	7.7	29	15	O71337	O71337 human endog
625	3	7.7	29	15	O71997	O71997 human endog
626	3	7.7	29	15	O71335	O71335 human endog
627	3	7.7	29	16	O25837	O25837 helicobacte

628	3	7.7	29	16	Q9KAV1	Q9kav1 bacillus ha
629	3	7.7	29	16	Q8ZP22	Q8zp22 salmonella
630	3	7.7	29	16	Q8ZL14	Q8zl14 salmonella
631	3	7.7	29	16	Q8X3T7	Q8x3t7 escherichia
632	3	7.7	29	16	Q8X3T6	Q8x3t6 escherichia
633	3	7.7	29	16	Q8X2E5	Q8x2e5 escherichia
634	3	7.7	29	16	Q8XU13	Q8xu13 ralstonia s
635	3	7.7	29	16	Q8PCQ6	Q8pcq6 xanthomonas
636	3	7.7	29	16	Q9X901	Q9x901 streptomyce
637	3	7.7	29	16	Q9S1T6	Q9s1t6 streptomyce
638	3	7.7	29	16	Q8EQ82	Q8eq82 oceanobacil
639	3	7.7	29	16	Q8DFV6	Q8dfv6 vibrio vuln
640	3	7.7	29	17	Q8ZTM0	Q8ztm0 pyrobaculum
641	3	7.7	30	1	Q9UWK8	Q9uwk8 thermococcu
642	3	7.7	30	2	Q85587	Q85587 chlamydia t
643	3	7.7	30	2	Q9R8H1	Q9r8h1 chlamydia t
644	3	7.7	30	2	Q85581	Q85581 chlamydia t
645	3	7.7	30	2	Q9R8F6	Q9r8f6 chlamydia t
646	3	7.7	30	2	Q8KYE4	Q8kye4 bacillus an
647	3	7.7	30	2	Q9R5A3	Q9r5a3 pseudomonas
648	3	7.7	30	2	Q9R4K2	Q9r4k2 campylobact
649	3	7.7	30	2	Q9R8G2	Q9r8g2 chlamydia t
650	3	7.7	30	2	Q9R8I9	Q9r8i9 chlamydia t
651	3	7.7	30	2	Q9R8I3	Q9r8i3 chlamydia t
652	3	7.7	30	2	Q9RZY9	Q9rzy9 borrelia bu
653	3	7.7	30	2	Q9L8F9	Q9l8f9 klebsiella
654	3	7.7	30	2	Q85563	Q85563 chlamydia t
655	3	7.7	30	2	Q9R8G5	Q9r8g5 chlamydia t
656	3	7.7	30	2	Q9R8E5	Q9r8e5 chlamydia t
657	3	7.7	30	2	Q9R4J2	Q9r4j2 helicobacte
658	3	7.7	30	2	Q9R8H5	Q9r8h5 chlamydia t
659	3	7.7	30	2	Q44171	Q44171 anabaena sp
660	3	7.7	30	2	Q9R8I5	Q9r8i5 chlamydia t
661	3	7.7	30	2	Q9R8F8	Q9r8f8 chlamydia t
662	3	7.7	30	2	Q9R8F3	Q9r8f3 chlamydia t
663	3	7.7	30	2	Q47355	Q47355 escherichia
664	3	7.7	30	2	Q9R8F4	Q9r8f4 chlamydia t
665	3	7.7	30	2	Q9R8G7	Q9r8g7 chlamydia t
666	3	7.7	30	2	Q9R8I1	Q9r8i1 chlamydia t
667	3	7.7	30	2	Q9R8J1	Q9r8j1 chlamydia t
668	3	7.7	30	2	Q9R4A9	Q9r4a9 clostridium
669	3	7.7	30	2	Q9R8H9	Q9r8h9 chlamydia t
670	3	7.7	30	2	Q9K532	Q9k532 listeria mo
671	3	7.7	30	2	Q93GF6	Q93gf6 staphylococ
672	3	7.7	30	2	Q9R8H3	Q9r8h3 chlamydia t
673	3	7.7	30	2	Q9R8G0	Q9r8g0 chlamydia t
674	3	7.7	30	2	Q9R8G1	Q9r8g9 chlamydiapp
675	3	7.7	30	2	Q9L8I9	Q9l8i9 enterobacte
676	3	7.7	30	2	Q9R530	Q9r530 escherichia
677	3	7.7	30	2	Q9R8H7	Q9r8h7 chlamydia t
678	3	7.7	30	2	Q9R5K3	Q9r5k3 leptospira
679	3	7.7	30	2	Q02800	Q02800 streptomyce
680	3	7.7	30	2	Q9R8I7	Q9r8i7 chlamydia t
681	3	7.7	30	2	Q9S014	Q9s014 borrelia bu
682	3	7.7	30	2	Q9R8F1	Q9r8f1 chlamydia t
683	3	7.7	30	2	Q9R4A8	Q9r4a8 clostridium
684	3	7.7	30	2	Q9RER6	Q9rer6 enterobacte

685	3	7.7	30	2	P83001	P83001 pseudomonas
686	3	7.7	30	2	P82134	P82134 corynebacte
687	3	7.7	30	2	Q8GQR2	Q8gqr2 bacillus my
688	3	7.7	30	2	Q8GQQ6	Q8gqq6 bacillus th
689	3	7.7	30	2	Q8GQQ4	Q8gqq4 bacillus th
690	3	7.7	30	2	Q8GF44	Q8gf44 zymomonas m
691	3	7.7	30	2	Q8G896	Q8g896 bacillus ce
692	3	7.7	30	2	Q8G895	Q8g895 bacillus ce
693	3	7.7	30	2	Q8G894	Q8g894 bacillus we
694	3	7.7	30	3	Q02213	Q02213 geotrichum
695	3	7.7	30	3	Q02176	Q02176 geotrichum
696	3	7.7	30	3	Q9URB6	Q9urb6 acremonium
697	3	7.7	30	4	Q16330	Q16330 homo sapien
698	3	7.7	30	4	Q96CZ0	Q96cz0 homo sapien
699	3	7.7	30	4	Q9UCW8	Q9ucw8 homo sapien
700	3	7.7	30	4	Q9UCW7	Q9ucw7 homo sapien
701	3	7.7	30	4	Q16113	Q16113 homo sapien
702	3	7.7	30	4	Q96D69	Q96d69 homo sapien
703	3	7.7	30	4	Q9UMJ2	Q9umj2 homo sapien
704	3	7.7	30	4	Q96Q60	Q96q60 homo sapien
705	3	7.7	30	4	Q14098	Q14098 homo sapien
706	3	7.7	30	4	Q99922	Q99922 homo sapien
707	3	7.7	30	4	Q9UBV5	Q9ubv5 homo sapien 50X,
708	3	7.7	30	4	Q9UC96	Q9uc96 hemof50apien
709	3	7.7	30	4	Q96FR0	Q96fr0 homo sapien
710	3	7.7	30	4	Q8WUP3	Q8wup3 homo sapien
711	3	7.7	30	4	Q9BWZ3	Q9bwz3 homo sapien
712	3	7.7	30	4	P78542	P78542 homo sapien
713	3	7.7	30	5	Q27545	Q27545 crithidia f
714	3	7.7	30	5	Q8WSM0	Q8wsm0 caenorhabdi
715	3	7.7	30	5	Q95PT1	Q95pt1 leishmania
716	3	7.7	30	5	Q9BM72	Q9bm72 drosophila
717	3	7.7	30	5	Q8I868	Q8i868 acanthamoeb
718	3	7.7	30	6	Q28321	Q28321 capra hircu
719	3	7.7	30	6	Q9TS67	Q9ts67 sus
720	3	7.7	30	6	Q95M52	Q95m52 bos taurus
721	3	7.7	30	6	Q28323	Q28323 capra hircu
722	3	7.7	30	6	Q9MZX0	Q9mzx0 colobus pol
723	3	7.7	30	6	Q8SPU1	Q8spu1 macaca mula
724	3	7.7	30	6	Q9TQQ6	Q9tqq6 canis famil
725	3	7.7	30	6	Q9TTF9	Q9ttf9 ateles belz
726	3	7.7	30	6	O46424	O46424 oryctolagus
727	3	7.7	30	8	Q9T2V9	Q9t2v9 cochliobolu
728	3	7.7	30	8	Q9MJF6	Q9mjf6 candida alb
729	3	7.7	30	8	Q8M0A1	Q8m0a1 bucorvus le
730	3	7.7	30	8	Q94TX1	Q94tx1 lithodes ma
731	3	7.7	30	8	Q9T2P9	Q9t2p9 narcissus p
732	3	7.7	30	8	Q34897	Q34897 lasiorhinus
733	3	7.7	30	8	Q8M2G1	Q8m2g1 vestiaria c
734	3	7.7	30	8	Q9T2P2	Q9t2p2 rattus sp.
735	3	7.7	30	8	Q95F79	Q95f79 hizikia fus
736	3	7.7	30	8	Q9TI56	Q9ti56 eucalyptus
737	3	7.7	30	9	Q8W674	Q8w674 enterobacte
738	3	7.7	30	10	Q9FQX4	Q9fqx4 oncidium cv
739	3	7.7	30	10	O23933	O23933 flaveria tr
740	3	7.7	30	10	Q93WY2	Q93wy2 oryza sativ
741	3	7.7	30	10	Q9FRA1	Q9fra1 oryza sativ

742	3	7.7	30	10	Q41490	Q41490 solanum tub
743	3	7.7	30	11	Q8K3D0	Q8k3d0 mus musculu
744	3	7.7	30	11	Q9QVC3	Q9qvc3 rattus sp.
745	3	7.7	30	11	Q9QV39	Q9qv39 rattus sp.
746	3	7.7	30	11	Q9QV43	Q9qv43 rattus sp.
747	3	7.7	30	11	Q8R4W3	Q8r4w3 mus musculu
748	3	7.7	30	11	Q8K4T8	Q8k4t8 rattus norv
749	3	7.7	30	11	Q8R4W4	Q8r4w4 mus musculu
750	3	7.7	30	11	Q9QV44	Q9qv44 mus sp. and
751	3	7.7	30	11	Q9JHC2	Q9jhc2 rattus norv
752	3	7.7	30	11	Q8K4T7	Q8k4t7 rattus norv
753	3	7.7	30	11	Q9WUS6	Q9wus6 mus musculu
754	3	7.7	30	11	Q9QV06	Q9qv06 rattus sp.
755	3	7.7	30	11	Q8BR32	Q8br32 mus musculu
756	3	7.7	30	12	Q9QS22	Q9qs22 hepatitis b
757	3	7.7	30	12	Q9QS36	Q9qs36 hepatitis b
758	3	7.7	30	12	Q9QS20	Q9qs20 hepatitis b
759	3	7.7	30	12	Q9QS16	Q9qs16 hepatitis b
760	3	7.7	30	12	Q9QS28	Q9qs28 hepatitis b
761	3	7.7	30	12	Q9QS53	Q9qs53 hepatitis b
762	3	7.7	30	12	Q9QS24	Q9qs24 hepatitis b
763	3	7.7	30	12	Q9QS43	Q9qs43 hepatitis b
764	3	7.7	30	12	Q9QS39	Q9qs39 hepatitis b
765	3	7.7	30	12	Q9QS13	Q9qs13 hepatitis b
766	3	7.7	30	12	Q9QS45	Q9qs45 hepatitis b
767	3	7.7	30	12	Q9QS47	Q9qs47 hepatitis b
768	3	7.7	30	12	Q9QS40	Q9qs40 hepatitis b
769	3	7.7	30	12	Q9QS14	Q9qs14 hepatitis b
770	3	7.7	30	12	Q9QS52	Q9qs52 hepatitis b
771	3	7.7	30	12	Q9QS33	Q9qs33 hepatitis b
772	3	7.7	30	12	Q9QS19	Q9qs19 hepatitis b
773	3	7.7	30	12	Q9QS51	Q9qs51 hepatitis b
774	3	7.7	30	12	Q91HB8	Q91hb8 tt virus. o
775	3	7.7	30	12	Q9QS29	Q9qs29 hepatitis b
776	3	7.7	30	12	Q9QS49	Q9qs49 hepatitis b
777	3	7.7	30	12	Q9QS50	Q9qs50 hepatitis b
778	3	7.7	30	12	Q9QS12	Q9qs12 hepatitis b
779	3	7.7	30	12	Q9QS37	Q9qs37 hepatitis b
780	3	7.7	30	12	Q9QS17	Q9qs17 hepatitis b
781	3	7.7	30	12	Q9QS32	Q9qs32 hepatitis b
782	3	7.7	30	12	Q9IJV5	Q9ijv5 norwalk vir
783	3	7.7	30	12	Q9QS48	Q9qs48 hepatitis b
784	3	7.7	30	12	Q9QS21	Q9qs21 hepatitis b
785	3	7.7	30	12	Q9QS27	Q9qs27 hepatitis b
786	3	7.7	30	12	Q9QS41	Q9qs41 hepatitis b
787	3	7.7	30	12	Q9QS15	Q9qs15 hepatitis b
788	3	7.7	30	12	Q9QS38	Q9qs38 hepatitis b
789	3	7.7	30	12	Q9QS30	Q9qs30 hepatitis b
790	3	7.7	30	12	Q86870	Q86870 cauliflower
791	3	7.7	30	12	Q9QS31	Q9qs31 hepatitis b
792	3	7.7	30	12	Q9QS11	Q9qs11 hepatitis b
793	3	7.7	30	12	Q9QS26	Q9qs26 hepatitis b
794	3	7.7	30	12	Q9QS46	Q9qs46 hepatitis b
795	3	7.7	30	12	Q66858	Q66858 foot-and-mo
796	3	7.7	30	12	Q9QS18	Q9qs18 hepatitis b
797	3	7.7	30	12	Q9QS44	Q9qs44 hepatitis b
798	3	7.7	30	12	Q9QS25	Q9qs25 hepatitis b

799	3	7.7	30	12	Q9QS34	Q9qs34 hepatitis b
800	3	7.7	30	12	Q9QS42	Q9qs42 hepatitis b
801	3	7.7	30	12	Q9WLK3	Q9wlk3 hepatitis e
802	3	7.7	30	12	Q66859	Q66859 foot-and-mo
803	3	7.7	30	12	Q96630	Q96630 bovine aden
804	3	7.7	30	12	Q9QS23	Q9qs23 hepatitis b
805	3	7.7	30	12	Q9QS35	Q9qs35 hepatitis b
806	3	7.7	30	13	Q9PRX3	Q9prx3 xenopus lae
807	3	7.7	30	13	Q9YGG6	Q9ygg6 xiphophorus
808	3	7.7	30	13	Q9YGG5	Q9ygg5 xiphophorus
809	3	7.7	30	13	Q9YGG2	Q9ygg2 xiphophorus
810	3	7.7	30	13	Q9YGF9	Q9ygf9 xiphophorus
811	3	7.7	30	13	Q9YGG7	Q9ygg7 xiphophorus
812	3	7.7	30	13	Q9YGG4	Q9ygg4 xiphophorus
813	3	7.7	30	13	Q9YGG3	Q9ygg3 xiphophorus
814	3	7.7	30	13	Q9YGD5	Q9ygd5 xiphophorus
815	3	7.7	30	15	P90307	P90307 human immun
816	3	7.7	30	15	Q86599	Q86599 human endog
817	3	7.7	30	15	Q9WJA9	Q9wja9 human immun
818	3	7.7	30	15	Q991P5	Q991p5 human immun
819	3	7.7	30	15	Q03514	Q03514 mouse intra
820	3	7.7	30	16	O24869	O24869 helicobacte
821	3	7.7	30	16	O50822	O50822 borrelia bu
822	3	7.7	30	16	O50910	O50910 borrelia bu
823	3	7.7	30	16	Q9X0W9	Q9x0w9 thermotoga
824	3	7.7	30	16	Q9X066	Q9x066 thermotoga
825	3	7.7	30	16	Q9WZ86	Q9wz86 thermotoga
826	3	7.7	30	16	Q9PA01	Q9pa01 xylella fas
827	3	7.7	30	16	Q9KV65	Q9kv65 vibrio chol
828	3	7.7	30	16	Q9KQQ5	Q9kqq5 vibrio chol
829	3	7.7	30	16	Q9KPR0	Q9kpr0 vibrio chol
830	3	7.7	30	16	Q9KNF2	Q9knf2 vibrio chol
831	3	7.7	30	16	Q9KLP5	Q9klp5 vibrio chol
832	3	7.7	30	16	Q9K7Y1	Q9k7y1 bacillus ha
833	3	7.7	30	16	Q9JUP4	Q9jup4 neisseria m
834	3	7.7	30	16	Q9I5K7	Q9i5k7 pseudomonas
835	3	7.7	30	16	Q98NK7	Q98nk7 rhizobium l
836	3	7.7	30	16	Q98LE7	Q98le7 rhizobium l
837	3	7.7	30	16	Q97SR7	Q97sr7 streptococc
838	3	7.7	30	16	Q97R13	Q97r13 streptococc
839	3	7.7	30	16	Q8X4J3	Q8x4j3 escherichia
840	3	7.7	30	16	Q99VB7	Q99vb7 staphylococ
841	3	7.7	30	16	Q8G1R1	Q8g1r1 brucella su
842	3	7.7	30	16	Q8G036	Q8g036 brucella su
843	3	7.7	30	16	Q8FZX9	Q8fxz9 brucella su
844	3	7.7	30	16	Q8FXU3	Q8fxu3 brucella su
845	3	7.7	30	16	Q8EKP1	Q8ekp1 shewanella
846	3	7.7	30	16	Q8EJS7	Q8ejs7 shewanella
847	3	7.7	30	16	Q8EJP3	Q8ejp3 shewanella
848	3	7.7	30	16	Q8EHK5	Q8ehk5 shewanella
849	3	7.7	30	16	Q8EG27	Q8eg27 shewanella
850	3	7.7	30	16	Q8EFH6	Q8efh6 shewanella
851	3	7.7	30	16	Q8ECK7	Q8eck7 shewanella
852	3	7.7	30	16	Q8EB32	Q8eb32 shewanella
853	3	7.7	30	16	Q8EAV6	Q8eav6 shewanella
854	3	7.7	30	16	Q8DZ13	Q8dz13 streptococc
855	3	7.7	30	16	Q8DS00	Q8ds00 streptococc

856	3	7.7	30	16	Q8CU88	Q8cu88 staphylococ
857	3	7.7	30	16	Q8CRR1	Q8crr1 staphylococ
858	3	7.7	30	16	Q8CKB0	Q8ckb0 yersinia pe
859	3	7.7	30	17	Q9HMB0	Q9hmb0 halobacteri
860	3	7.7	30	17	Q8ZVL0	Q8zvl0 pyrobaculum
861	3	7.7	31	1	Q8X254	Q8x254 halobacteri
862	3	7.7	31	2	Q54825	Q54825 streptococc
863	3	7.7	31	2	Q53449	Q53449 chlamydia t
864	3	7.7	31	2	Q9K4X1	Q9k4x1 planktothri
865	3	7.7	31	2	Q9S619	Q9s619 prochloroco
866	3	7.7	31	2	Q9L7N5	Q9l7n5 borrelia bi
867	3	7.7	31	2	Q9S0E6	Q9s0e6 borrelia bu
868	3	7.7	31	2	Q9X3C3	Q9x3c3 prochloroco
869	3	7.7	31	2	Q47374	Q47374 escherichia
870	3	7.7	31	2	Q9R2N7	Q9r2n7 escherichia
871	3	7.7	31	2	Q9K4X9	Q9k4x9 planktothri
872	3	7.7	31	2	Q9F1I5	Q9f1i5 enterococcu
873	3	7.7	31	2	Q8KYP8	Q8kyp8 bacillus an
874	3	7.7	31	2	Q9R503	Q9r503 thermotoga
875	3	7.7	31	2	Q9L7N3	Q9l7n3 borrelia an
876	3	7.7	31	2	Q47353	Q47353 escherichia
877	3	7.7	31	2	Q9RHP1	Q9rhp1 escherichia
878	3	7.7	31	2	Q8RTS5	Q8rts5 uncultured
879	3	7.7	31	2	Q9R2G0	Q9r2g0 staphylococ
880	3	7.7	31	2	Q52917	Q52917 rhizobium m
881	3	7.7	31	2	Q53411	Q53411 bacillus su
882	3	7.7	31	2	Q32325	Q32325 clostridium
883	3	7.7	31	2	Q8L3M4	Q8l3m4 rickettsia
884	3	7.7	31	2	Q69420	Q69420 escherichia
885	3	7.7	31	2	Q9EV62	Q9ev62 streptococc
886	3	7.7	31	2	Q47364	Q47364 escherichia
887	3	7.7	31	2	Q44263	Q44263 aeromonas s
888	3	7.7	31	2	Q49248	Q49248 mycoplasma
889	3	7.7	31	3	Q94120	Q94120 saccharomyc
890	3	7.7	31	4	4Q9UMG3	Q9umg3 o sapien
891	3	7.7	31	4	Q9BQU1	Q9bqu1 homo sapien
892	3	7.7	31	4	Q8N6N1	Q8n6n1 homo sapien
893	3	7.7	31	4	Q9UCF2	Q9ucf2 homo sapien
894	3	7.7	31	4	Q9UJ40	Q9uj40 homo sapien
895	3	7.7	31	4	Q9UEI3	Q9uei3 homo sapien
896	3	7.7	31	4	Q9Y2A3	Q9y2a3 homo sapien
897	3	7.7	31	4	Q8NEI8	Q8nei8 homo sapien
898	3	7.7	31	4	Q9UDK2	Q9udk2 homo sapien
899	3	7.7	31	4	Q8WYF5	Q8wyf5 homo sapien
900	3	7.7	31	4	Q96FE4	Q96fe4 homo sapien
901	3	7.7	31	4	Q8WYF3	Q8wyf3 homo sapien
902	3	7.7	31	4	Q8N5X3	
903	3	7.7	31	4	Q99893	Q99893 homo sapien
904	3	7.7	31	4	Q9UBW3	Q9ubw3 homo sapien
905	3	7.7	31	4	Q96Q71	Q96q71 homo sapien
906	3	7.7	31	4	Q8TBX1	Q8tbx1 homo sapien
907	3	7.7	31	5	Q19924	Q19924 caenorhabdi
908	3	7.7	31	5	Q26760	Q26760 trypanosoma
909	3	7.7	31	5	Q26761	Q26761 trypanosoma
910	3	7.7	31	5	Q26762	Q26762 trypanosoma
911	3	7.7	31	5	Q8STH5	Q8sth5 drosophila
912	3	7.7	31	5	Q9NGN5	Q9ngn5 strongyloce

913	3	7.7	31	5	Q17165	Q17165 brugia mala
914	3	7.7	31	5	Q8IF28	Q8if28 trypanosoma
915	3	7.7	31	5	Q8IEY3	Q8iey3 trypanosoma
916	3	7.7	31	6	Q9TRJ3	Q9trj3 canis famil
917	3	7.7	31	6	Q28325	Q28325 capra hircu
918	3	7.7	31	6	Q9TR79	Q9tr79 ovis aries
919	3	7.7	31	6	Q9GLD6	Q9gld6 sus scrofa
920	3	7.7	31	6	Q9BEI0	Q9bei0 monodelphis
921	3	7.7	31	6	Q9BDF3	Q9bdf3 orycteropus
922	3	7.7	31	6	Q9XS80	Q9xs80 sus scrofa
923	3	7.7	31	6	Q9TR61	Q9tr61 canis famil
924	3	7.7	31	6	Q9TSE4	Q9tse4 oryctolagus
925	3	7.7	31	6	Q9GJZ3	Q9gjz3 dugong dugo
926	3	7.7	31	7	Q29868	Q29868 homo sapien
927	3	7.7	31	7	Q9MWI7	Q9mwi7 geospiza sc
928	3	7.7	31	8	Q9T690	Q9t690 gecko gecko
929	3	7.7	31	8	Q8MBD7	Q8mbd7 astripomoea
930	3	7.7	31	8	Q9MNM2	Q9mnm2 bufo americ
931	3	7.7	31	8	Q36709	Q36709 ophiopholis
932	3	7.7	31	8	Q94NH2	Q94nh2 littorina s
933	3	7.7	31	8	Q9MS68	Q9ms68 euglena des
934	3	7.7	31	8	Q33577	Q33577 trypanosoma
935	3	7.7	31	8	Q9TKW5	Q9tkw5 nephroselmi
936	3	7.7	31	8	Q8MB91	Q8mb91 convolvulus
937	3	7.7	31	9	Q9B083	Q9b083 mycobacteri
938	3	7.7	31	9	Q64265	Q64265 mycobacteri
939	3	7.7	31	10	Q9SPF4	Q9spf4 vitis vinif
940	3	7.7	31	10	Q9M3S3	Q9m3s3 arabidopsis
941	3	7.7	31	10	Q8LMG1	Q8lmg1 oryza sativ
942	3	7.7	31	10	Q9SPF5	Q9spf5 vitis vinif
943	3	7.7	31	11	Q9QVA5	Q9qva5 cavia (guin
944	3	7.7	31	11	Q9QXB6	Q9qxb6 mus musculu
945	3	7.7	31	11	Q9ESY0	Q9esy0 mus musculu
946	3	7.7	31	11	Q99KK6	Q99kk6 mus musculu
947	3	7.7	31	11	Q9WUS8	Q9wus8 mus musculu
948	3	7.7	31	11	Q99PC8	Q99pc8 rattus norv
949	3	7.7	31	11	Q92ZZ6	Q92zz6 mus musculu
950	3	7.7	31	11	Q9QYY4	Q9qyy4 mus musculu
951	3	7.7	31	11	Q8CGM7	Q8cgm7 mus musculu
952	3	7.7	31	12	Q8JSB4	Q8jsb4 hepatitis b
953	3	7.7	31	12	Q68024	Q68024 hepatitis b
954	3	7.7	31	12	Q8JS95	Q8js95 hepatitis b
955	3	7.7	31	12	Q67979	Q67979 hepatitis b
956	3	7.7	31	12	Q8JSB3	Q8jsb3 hepatitis b
957	3	7.7	31	12	Q68058	Q68058 hepatitis b
958	3	7.7	31	12	Q8JS78	Q8js78 hepatitis b
959	3	7.7	31	12	Q8JS97	Q8js97 hepatitis b
960	3	7.7	31	12	Q68049	Q68049 hepatitis b
961	3	7.7	31	12	Q67967	Q67967 hepatitis b
962	3	7.7	31	12	Q8JS90	Q8js90 hepatitis b
963	3	7.7	31	12	Q8JSB0	Q8jsb0 hepatitis b
964	3	7.7	31	12	Q8JSC6	Q8jsc6 hepatitis b
965	3	7.7	31	12	Q67987	Q67987 hepatitis b
966	3	7.7	31	12	Q8JSB7	Q8jsb7 hepatitis b
967	3	7.7	31	12	Q8JS83	Q8js83 hepatitis b
968	3	7.7	31	12	Q67992	Q67992 hepatitis b
969	3	7.7	31	12	Q68080	Q68080 hepatitis b

970	3	7.7	31	12	Q68002	Q68002 hepatitis b
971	3	7.7	31	12	Q68013	Q68013 hepatitis b
972	3	7.7	31	12	Q8JS98	Q8js98 hepatitis b
973	3	7.7	31	12	Q68050	Q68050 hepatitis b
974	3	7.7	31	12	Q8JSB6	Q8jsb6 hepatitis b
975	3	7.7	31	12	Q68004	Q68004 hepatitis b
976	3	7.7	31	12	Q8JS93	Q8js93 hepatitis b
977	3	7.7	31	12	Q8JSA4	Q8jsa4 hepatitis b
978	3	7.7	31	12	Q8JS84	Q8js84 hepatitis b
979	3	7.7	31	12	Q68019	Q68019 hepatitis b
980	3	7.7	31	12	Q73430	Q73430 human papil
981	3	7.7	31	12	Q9PXL2	Q9pxl2 hepatitis b
982	3	7.7	31	12	Q8JSA0	Q8jsa0 hepatitis b
983	3	7.7	31	12	Q8JSD5	Q8jsd5 hepatitis b
984	3	7.7	31	12	Q67998	Q67998 hepatitis b
985	3	7.7	31	12	Q68056	Q68056 hepatitis b
986	3	7.7	31	12	Q68033	Q68033 hepatitis b
987	3	7.7	31	12	Q68018	Q68018 hepatitis b
988	3	7.7	31	12	Q68011	Q68011 hepatitis b
989	3	7.7	31	12	Q8JS74	Q8js74 hepatitis b
990	3	7.7	31	12	Q8JS66	Q8js66 hepatitis b
991	3	7.7	31	12	Q68071	Q68071 hepatitis b
992	3	7.7	31	12	Q8JS81	Q8js81 hepatitis b
993	3	7.7	31	12	Q67957	Q67957 hepatitis b
994	3	7.7	31	12	Q67983	Q67983 hepatitis b
995	3	7.7	31	12	Q67985	Q67985 hepatitis b
996	3	7.7	31	12	Q67962	Q67962 hepatitis b
997	3	7.7	31	12	Q67990	Q67990 hepatitis b
998	3	7.7	31	12	Q68034	Q68034 hepatitis b
999	3	7.7	31	12	Q68046	Q68046 hepatitis b
1000	3	7.7	31	12	Q68000	Q68000 hepatitis b

ALIGNMENTS

RESULT 1

Q8P6H8

ID Q8P6H8 PRELIMINARY; PRT; 37 AA.

AC Q8P6H8;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Phage-related protein.

GN ORF52 OR XCC2991.

OS Xanthomonas campestris (pv. campestris).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=340;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33913 / NCPPB 528;

RX MEDLINE=22022145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE012413; AAM42263.1; -.
KW Complete proteome.
SQ SEQUENCE 37 AA; 4295 MW; 41E2614125B1A922 CRC64;

Query Match 15.4%; Score 6; DB 16; Length 37;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERARL 16
|||||
Db 27 RERARL 32

RESULT 2

Q8FVK2
ID Q8FVK2 PRELIMINARY; PRT; 38 AA.
AC Q8FVK2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN BRA0835.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
DR EMBL; AE014577; AAN34010.1; -.
DR TIGR; BRA0835; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 38 AA; 4255 MW; D71AA8D253FD7F86 CRC64;

Query Match 15.4%; Score 6; DB 16; Length 38;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ERARLL 17
|||||
Db 6 ERARLL 11

RESULT 3

Q9TWE2

ID Q9TWE2 PRELIMINARY; PRT; 28 AA.
AC Q9TWE2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE AXONEMAL alpha-tubulin isoform (Fragment).
OS Paracentrotus lividus (Common sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
OC Paracentrotus.
OX NCBI_TaxID=7656;
RN [1]
RP SEQUENCE.
RX MEDLINE=96215272; PubMed=8626629;
RA Mary J., Redeker V., Le Caer J.P., Rossier J., Schmitter J.M.;
RT "Posttranslational modifications in the C-terminal tail of axonemal
RT tubulin from sea urchin sperm.";
RL J. Biol. Chem. 271:9928-9933(1996).
SQ SEQUENCE 28 AA; 3104 MW; 9C50E220D1AFD7C1 CRC64;

Query Match 12.8%; Score 5; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAALE 21
|||||
Db 2 LAALE 6

RESULT 4

Q9WTS1

ID Q9WTS1 PRELIMINARY; PRT; 28 AA.
AC Q9WTS1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Egfr (Fragment).
GN EGFR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Kondoh S.K., Akiyama N.;

RT "Rat EGFR promoter from NRK cells.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB025197; BAA76391.1; -.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 2855 MW; B56EAB41A074D15A CRC64;

Query Match 12.8%; Score 5; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
|||||
Db 14 LLAAL 18

RESULT 5
Q9TTP2
ID Q9TTP2 PRELIMINARY; PRT; 29 AA.
AC Q9TTP2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Alanine glyoxylate aminotransferase (EC 2.6.1.44) (Fragment).
GN AGT.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20188798; PubMed=10723739;
RA Holbrook J.D., Birdsey G.M., Yang Z., Bruford M.W., Danpure C.J.;
RT "Molecular adaptation of alanine Glyoxylate aminotransferase targeting
RT in primates.";
RL Mol. Biol. Evol. 17:387-400(2000).
DR EMBL; AJ237886; CAB56803.1; -.
KW Aminotransferase; Transferase.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3048 MW; 51645B5E27835DC3 CRC64;

Query Match 12.8%; Score 5; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 HKLLV 35
|||||
Db 4 HKLLV 8

RESULT 6
Q9JLR6
ID Q9JLR6 PRELIMINARY; PRT; 29 AA.
AC Q9JLR6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Epidermal growth factor receptor (Fragment).

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Spleen;
RX MEDLINE=20167208; PubMed=10702298;
RA Liu X.-W., Katagiri Y., Jiang H., Gong L.-J., Guo L.-Y., Shibutani M.,
RA Johnson A.C., Guroff G.;
RT "Cloning and Characterization of the Promoter Region of the Rat
RT Epidermal Growth Factor Receptor Gene and Its Transcriptional
RT Regulation by Nerve Growth Factor in PC12 Cells.";
RL J. Biol. Chem. 275:7280-7288 (2000).
DR EMBL; AF142153; AAF27540.1; -.
KW Receptor.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 2984 MW; 1A056EAB41A074D1 CRC64;

Query Match 12.8%; Score 5; DB 11; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
|||||
Db 14 LLAAL 18

RESULT 7

Q9I390
ID Q9I390 PRELIMINARY; PRT; 29 AA.
AC Q9I390;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE KdpF protein.
GN KDPF OR PA1632.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964 (2000).
DR EMBL; AE004591; AAG05021.1; -.
KW Complete proteome.
SQ SEQUENCE 29 AA; 3206 MW; 031E034AF96C0392 CRC64;

Query Match 12.8%; Score 5; DB 16; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALA 5
|||
Db 8 SLALA 12

RESULT 8

Q9RHF9
ID Q9RHF9 PRELIMINARY; PRT; 31 AA.
AC Q9RHF9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Periplasmic mercuric ion binding protein (Fragment).
GN MERP.
OS Acinetobacter calcoaceticus.
OG Plasmid pKLH1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=471;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=aberrant mercury resistance transposon;
RA Kholodii G.Y., Mindlin S.Z., Lomovskaya O.L., Gorlenko Z.M.,
RA Yurieva O.V., Nikiforov V.G.;
RT "pKLH1-like aberrant mercury resistance transposons of environmental
RT Acinetobacter strains: spread, polymorphism and possible origin.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ251517; CAB65941.1; -.
DR InterPro; IPR001802; HG_scavenger.
DR PRINTS; PR00946; HGSCAVENGER.
KW Plasmid.
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3182 MW; 2EBCF50B7D9BC66E CRC64;

Query Match 12.8%; Score 5; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALA 5
|||
Db 7 SLALA 11

RESULT 9

Q9T1K0
ID Q9T1K0 PRELIMINARY; PRT; 31 AA.
AC Q9T1K0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Shiga toxin A subunit (EC 3.2.2.22) (rRNA N-glycosidase)
(Fragment).

GN STX2.
OS Bacteriophage F6.
OC Viruses.
OX NCBI_TaxID=108918;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F6;
RX MEDLINE=98320580; PubMed=9647813;
RA Muniesa M., Jofre J.;
RT "Abundance in sewage of bacteriophages that infect Escherichia coli O157:H7 and that carry the Shiga toxin 2 gene.";
RL Appl. Environ. Microbiol. 64:2443-2448(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=F6;
RX MEDLINE=20117821; PubMed=10650226;
RA Muniesa M., Jofre J.;
RT "Occurrence of phages infecting Escherichia coli O157:H7 carrying the Stx 2 gene in sewage from different countries.";
RL FEMS Microbiol. Lett. 183:197-200(2000).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AJ251234; CAB61566.1; -.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
KW Hydrolase; Toxin.
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3414 MW; 99DB1A17091655B0 CRC64;

Query Match 12.8%; Score 5; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AALER 22
|||||
Db 14 AALER 18

RESULT 10
Q9T1K2
ID Q9T1K2 PRELIMINARY; PRT; 31 AA.
AC Q9T1K2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Shiga toxin A subunit (EC 3.2.2.22) (rRNA N-glycosidase)
DE (Fragment).
GN STX2.
OS Bacteriophage F3.
OC Viruses.
OX NCBI_TaxID=108916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F3;
RX MEDLINE=98320580; PubMed=9647813;
RA Muniesa M., Jofre J.;

RT "Abundance in sewage of bacteriophages that infect Escherichia coli
RT O157:H7 and that carrythe Shiga toxin 2 gene.";
RL Appl. Environ. Microbiol. 64:2443-2448(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=F3;
RX MEDLINE=20117821; PubMed=10650226;
RA Muniesa M., Jofre J.;
RT "Occurrence of phages infecting Escherichia coli O157:H7 carrying the
RT Stx 2 gene in sewage from different countries.";
RL FEMS Microbiol. Lett. 183:197-200(2000).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AJ251232; CAB61564.1; --.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
KW Hydrolase; Toxin.
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3414 MW; 99DB1A17091655B0 CRC64;

Query Match 12.8%; Score 5; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AALER 22
|||||
Db 14 AALER 18

RESULT 11
Q9T1K1
ID Q9T1K1 PRELIMINARY; PRT; 31 AA.
AC Q9T1K1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Shiga toxin A subunit (EC 3.2.2.22) (rRNA N-glycosidase)
DE (Fragment).
GN STX2.
OS Bacteriophage F5.
OC Viruses.
OX NCBI_TaxID=108917;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F5;
RX MEDLINE=98320580; PubMed=9647813;
RA Muniesa M., Jofre J.;
RT "Abundance in sewage of bacteriophages that infect Escherichia coli
RT O157:H7 and that carrythe Shiga toxin 2 gene.";
RL Appl. Environ. Microbiol. 64:2443-2448(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=F5;
RX MEDLINE=20117821; PubMed=10650226;
RA Muniesa M., Jofre J.;
RT "Occurrence of phages infecting Escherichia coli O157:H7 carrying the

RT Stx 2 gene in sewage from different countries.";
 RL FEMS Microbiol. Lett. 183:197-200(2000).
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AJ251233; CAB61565.1; -.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 KW Hydrolase; Toxin.
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3414 MW; 99DB1A17091655B0 CRC64;

 Query Match 12.8%; Score 5; DB 9; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 18 AALER 22
 |||||
 Db 14 AALER 18

RESULT 12
 Q9T1K3
 ID Q9T1K3 PRELIMINARY; PRT; 31 AA.
 AC Q9T1K3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Shiga toxin A subunit (EC 3.2.2.22) (rRNA N-glycosidase)
 DE (Fragment).
 GN STX2.
 OS Bacteriophage f1.
 OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
 OX NCBI_TaxID=10863;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F1;
 RX MEDLINE=98320580; PubMed=9647813;
 RA Muniesa M., Jofre J.;
 RT "Abundance in sewage of bacteriophages that infect Escherichia coli
 RT 0157:H7 and that carry the Shiga toxin 2 gene.";
 RL Appl. Environ. Microbiol. 64:2443-2448(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F1;
 RX MEDLINE=20117821; PubMed=10650226;
 RA Muniesa M., Jofre J.;
 RT "Occurrence of phages infecting Escherichia coli 0157:H7 carrying the
 RT Stx 2 gene in sewage from different countries.";
 RL FEMS Microbiol. Lett. 183:197-200(2000).
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AJ251231; CAB61563.1; -.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 KW Hydrolase; Toxin.

FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3414 MW; 99DB1A17091655B0 CRC64;

Query Match 12.8%; Score 5; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AALER 22
|||||
Db 14 AALER 18

RESULT 13
Q9KM83
ID Q9KM83 PRELIMINARY; PRT; 33 AA.
AC Q9KM83;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein VCA0500.
GN VCA0500.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E1 Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004381; AAF96403.1; -.
DR TIGR; VCA0500; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 33 AA; 3731 MW; 625DB1FF2E10E8A0 CRC64;

Query Match 12.8%; Score 5; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DDAAF 10
|||||
Db 16 DDAAF 20

RESULT 14
Q8XY48
ID Q8XY48 PRELIMINARY; PRT; 33 AA.
AC Q8XY48;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Probable phage-related protein fragment.
GN RSC1915 OR RS03485.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siquier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646067; CAD15617.1; -.
KW Complete proteome.
SQ SEQUENCE 33 AA; 4036 MW; 41DF9B7705EC474D CRC64;

Query Match 12.8%; Score 5; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERAR 15
|||||
Db 22 RERAR 26

RESULT 15
Q27372
ID Q27372 PRELIMINARY; PRT; 37 AA.
AC Q27372;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE (Clone 11) U1 snRNA, 3' end of CDS (Fragment).
GN U1 SNRNA.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96111299; PubMed=8589846;
RA Gao J.P., Herrera R.J.;
RT "U1 snRNA variants coexist in Bombyx mori cells.";
RL Insect Mol. Biol. 4:193-202(1995).
DR EMBL; L42957; AAB00485.1; -.
DR EMBL; L42955; AAB00483.1; -.
FT NON_TER 1 1

SQ SEQUENCE 37 AA; 4187 MW; 2541733F7C9D68FA CRC64;
Query Match 12.8%; Score 5; DB 5; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RARLL 17
|||||
Db 10 RARLL 14

RESULT 16

Q8SYH5
ID Q8SYH5 PRELIMINARY; PRT; 37 AA.
AC Q8SYH5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE RE58095p.
GN BCDNA:RE58095.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY071546; AAL49168.1; -.
DR FlyBase; FBgn0047081; BCDNA:RE58095.
SQ SEQUENCE 37 AA; 4505 MW; 98148EB2DD00287C CRC64;

Query Match 12.8%; Score 5; DB 5; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERAR 15
|||||
Db 20 RERAR 24

RESULT 17

Q9TTR4
ID Q9TTR4 PRELIMINARY; PRT; 37 AA.
AC Q9TTR4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Alanine glyoxylate aminotransferase (EC 2.6.1.44) (Fragment).
GN AGT.

OS Cercopithecus diana (Diana monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=36224;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=);
 RX MEDLINE=20188798; PubMed=10723739;
 RA Holbrook J.D., Birdsey G.M., Yang Z., Bruford M.W., Danpure C.J.;
 RT "Molecular adaptation of alanine Glyoxylate aminotransferase targeting
 in primates.";
 RL Mol. Biol. Evol. 17:387-400(2000).
 DR EMBL; AJ237891; CAB56774.1; -.
 KW Aminotransferase; Transferase.
 FT NON_TER 37 37
 SQ SEQUENCE 37 AA; 3979 MW; 7289022410A60DF1 CRC64;

 Query Match 12.8%; Score 5; DB 6; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 31 HKLLV 35
 |||||
 Db 4 HKLLV 8

RESULT 18
 Q9N260
 ID Q9N260 PRELIMINARY; PRT; 37 AA.
 AC Q9N260;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE MADH4 protein (Fragment).
 GN MADH4.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20118593; PubMed=10654432;
 RA Kelly K.A., Larsen N.J., Marklund S., Rothschild M.F.;
 RT "Mapping of two tumor suppressor genes in the pig.";
 RL Anim. Biotechnol. 10:81-85(1999).
 DR EMBL; AF120280; AAF70206.1; -.
 DR HSSP; Q13485; 1YGS.
 DR InterPro; IPR001132; Dwarfin.
 DR Pfam; PF03166; MH2; 1.
 FT NON_TER 1 1
 FT NON_TER 37 37
 SQ SEQUENCE 37 AA; 4038 MW; EDFA3087D75E7B30 CRC64;

Query Match 12.8%; Score 5; DB 6; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ERARL 16
 |||||
Db 26 ERARL 30

RESULT 19

Q9H4Y8

ID Q9H4Y8 PRELIMINARY; PRT; 38 AA.
AC Q9H4Y8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE DJ1041C10.1 (Beta-1,4-galactosyltransferase, polypeptide 5) (Beta-1,4-galactosyltransferase V) (Fragment).
GN B4GALT5 OR GT-V.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Heath P.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Sato T.;
RT "Promoter analysis of human beta-1,4-galactosyltransferase V gene.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL162615; CAC11145.1; -.
DR EMBL; AB067772; BAC07182.1; -.
KW Glycosyltransferase; Transferase.
FT NON_TER 38 38
SQ SEQUENCE 38 AA; 4359 MW; ECC7FA6515263101 CRC64;

Query Match 12.8%; Score 5; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
 |||||
Db 15 LLAAL 19

RESULT 20

Q8U580

ID Q8U580 PRELIMINARY; PRT; 38 AA.
AC Q8U580;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AGR_C_3308p.
GN AGR_C_3308.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.

OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quroollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328 (2001).
DR EMBL; AE008101; AAK87568.1; -.
SQ SEQUENCE 38 AA; 4583 MW; 9D7E1BD01CDC0F78 CRC64;

Query Match 12.8%; Score 5; DB 16; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 KLLVL 36
|||
Db 16 KLLVL 20

RESULT 21
Q9LB47
ID Q9LB47 PRELIMINARY; PRT; 39 AA.
AC Q9LB47;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vacuolating cytotoxin (Fragment).
GN VACA.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G21;
RA Ji X., Telford J.L., Burroni D., Guidotti S., Pagliaccia C.,
RA Rayrat J.M., Xu G., Rappuoli R.;
RT "Allelic variation of vacA gene in the Chinese Helicobacter pylori.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF050405; AAF26587.1; -.
DR InterPro; IPR003842; VacA.
DR PRINTS; PR01656; VACCYTOTOXIN.
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4308 MW; 18CA80FCE9D4C92C CRC64;

Query Match 12.8%; Score 5; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLALA 5
|||

Db 16 SLALA 20

RESULT 22

Q9UDI2
ID Q9UDI2 PRELIMINARY; PRT; 39 AA.
AC Q9UDI2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Neutrophil cytosolic factor 3; NCF-3 (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93277853; PubMed=8504089;
RA Kwong C.H., Malech H.L., Rotrosen D., Leto T.L.;
RT "Regulation of the human neutrophil NADPH oxidase by rho-related G-
RT proteins.";
RL Biochemistry 32:5711-5717(1993).
DR HSSP; P25763; 1A4R.
FT NON_TER 1 1
FT NON_CONS 11 12
FT NON_CONS 22 23
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4405 MW; 591520724F66E350 CRC64;

Query Match 12.8%; Score 5; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAALE 21
| | | |
Db 30 LAALE 34

RESULT 23

061645
ID 061645 PRELIMINARY; PRT; 39 AA.
AC 061645;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Alpha-tubulin (Fragment).
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
OC Aplysioidae; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RA Sung Y.J., Zhu D.F., Ambron R.T.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF055329; AAC12647.1; -.
FT NON_TER 1 1

SQ SEQUENCE 39 AA; 4393 MW; 0D3A0EB30DFC29AF CRC64;
Query Match 12.8%; Score 5; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 17 LAALE 21
|||||
Db 12 LAALE 16

RESULT 24
Q9ZKK1
ID Q9ZKK1 PRELIMINARY; PRT; 39 AA.
AC Q9ZKK1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Orf24.5.
OS Bacteriophage phi CTX.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=35343;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=phiCTX-c;
RA Hayashi T.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=phiCTX-c;
RX MEDLINE=99157549; PubMed=10027959;
RA Nakayama K., Kanaya S., Ohnishi M., Terawaki Y., Hayashi T.;
RT "The complete nucleotide sequence of phiCTX, a cytotoxin-converting
RT phage of *Pseudomonas aeruginosa*: implications for phage evolution and
RT horizontal gene transfer via bacteriophage.";
RL Mol. Microbiol. 31:399-419(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=phiCTX-c;
RX MEDLINE=90014160; PubMed=2507866;
RA Hayashi T., Kamio Y., Hishinuma F., Usami Y., Titani K., Terawaki Y.;
RT "*Pseudomonas aeruginosa* cytotoxin; the nucleotide sequence of the gene
RT and the mechanism of activation of the protoxin.";
RL Mol. Microbiol. 3:861-868(1989).
DR EMBL; AB008550; BAA36252.1; -.
SQ SEQUENCE 39 AA; 4587 MW; C9100CE65CF14BBE CRC64;

Query Match 12.8%; Score 5; DB 9; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 RERAR 15
|||||
Db 27 RERAR 31

RESULT 25

Q9ZRY5

ID Q9ZRY5 PRELIMINARY; PRT; 39 AA.
AC Q9ZRY5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Phosphoribosylpyrophosphate amidotransferase (Fragment).
GN PRAT.
OS Prunus avium (Cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=42229;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitts H.B., Coutts R.H.A.;
RL Plant Mol. Biol. 40:531-531(1999).
DR EMBL; AJ011797; CAA09786.1; -.
KW Transferase.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4244 MW; 06343203D5C3778F CRC64;

Query Match 12.8%; Score 5; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLALA 5
|||||
Db 11 SLALA 15

RESULT 26

Q9PXW1
ID Q9PXW1 PRELIMINARY; PRT; 39 AA.
AC Q9PXW1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE REV regulatory protein (Fragment).
OS Simian immunodeficiency virus SIVmac.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11711;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93276581; PubMed=7684879;
RA Benichou S., Venet A., Beyer C., Tiollais P., Madaule P.;
RT "Characterization of B-cell epitopes in the envelope glycoproteins of
RT simian immunodeficiency virus.";
RL Virology 194:870-874(1993).
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
SQ SEQUENCE 39 AA; 4892 MW; CB1C6F359A3D037D CRC64;

Query Match 12.8%; Score 5; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALAD 6
 |||||
Db 23 LALAD 27

RESULT 27

Q8F6J1

ID Q8F6J1 PRELIMINARY; PRT; 39 AA.
AC Q8F6J1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN LA1315.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AE011311; AAN48514.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 39 AA; 4720 MW; 2E6008943ADC3BF9 CRC64;

Query Match 12.8%; Score 5; DB 16; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 KLLVL 36
 |||||
Db 11 KLLVL 15

RESULT 28

Q8NHY1

ID Q8NHY1 PRELIMINARY; PRT; 28 AA.
AC Q8NHY1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hepatic nuclear factor 4 alpha (Fragment).
GN HNF4A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21592951; PubMed=11717395;
RA Boj S.F., Parrizas M., Maestro M.A., Ferrer J.;
RT "A transcription factor regulatory circuit in differentiated
pancreatic cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:14481-14486 (2001).
RN [2]

RP SEQUENCE FROM N.A.
RA Boj S.F., Parrizas M., Ferrer J.;
RT "HNF4A expression in human pancreatic cells.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF509467; AAM34296.1; -.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3003 MW; 0F314BDCBC5D2958 CRC64;

Query Match 10.3%; Score 4; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RERA 14
|||
Db 15 RERA 18

RESULT 29
Q8MJG7
ID Q8MJG7 PRELIMINARY; PRT; 28 AA.
AC Q8MJG7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Aldo-keto reductase family 1 member C2 (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Nonneman D.J., Rohrer G.A.;
RT "Comparative mapping of a region on chromosome 10q containing QTL for
reproduction in swine.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF473815; AAM70050.1; -.
DR InterPro; IPR001395; Aldo/ket_red.
DR Pfam; PF00248; aldo_ket_red; 1.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3008 MW; D319BA9C0D27F7A4 CRC64;

Query Match 10.3%; Score 4; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AALE 21
|||
Db 13 AALE 16

RESULT 30
Q95L33
ID Q95L33 PRELIMINARY; PRT; 28 AA.
AC Q95L33;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Potassium chloride cotransporter SLC12A4 (Fragment).
GN SLC12A4.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Hanzawa K., Lear T.L., Bailey E.;
RT "Mapping of equine potassium chloride cotransporter (SLC12A4) and
RT amino acid transporters (SLC7A10 and SLC7A9) and analysis for effect
RT of polymorphism on osmotic fragility of red blood cells.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF425260; AAL18852.1; -.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3364 MW; F2D772124C232F5C CRC64;

Query Match 10.3%; Score 4; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 LLVL 36
|||
Db 12 LLVL 15

RESULT 31
P92760
ID P92760 PRELIMINARY; PRT; 28 AA.
AC P92760;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit I (Fragment).
GN ND1.
OS Uromastyx acanthinura.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Uromastyicinae;
OC Uromastyx.
OX NCBI_TaxID=52167;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153826; PubMed=9000757;
RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
RT "Two novel gene orders and the role of light-strand replication in
RT rearrangement of the vertebrate mitochondrial genome.";
RL Mol. Biol. Evol. 14:91-104(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
RT structures of mitochondrial transfer RNAs.";
RL Mol. Biol. Evol. 14:30-39(1997).

DR EMBL; U71325; AAC62247.1; -.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 28 AA; 3057 MW; 4A37F11E5C4EEDAE CRC64;

Query Match 10.3%; Score 4; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
|||
Db 20 LAAL 23

RESULT 32
Q9QVC9
ID Q9QVC9 PRELIMINARY; PRT; 28 AA.
AC Q9QVC9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Glutathione S-transferase subunit YX, GST subunit YX (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92231842; PubMed=1567376;
RA Igarashi T., Tsuchiya T., Shikata Y., Sagami F., Tagaya O., Horie T.,
RA Satoh T.;
RT "Developmental aspects of a unique glutathione S-transferase subunit
RT Yx in the liver cytosol from rats with hereditary hyperbilirubinuria.
RT Comparison with rat fetal liver transferase subunit Yfetus.";
RL Biochem. J. 283:307-311(1992).
DR HSSP; P24472; 1GUK.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF02798; GST_N; 1.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3137 MW; 2C0CE25C09F0216F CRC64;

Query Match 10.3%; Score 4; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAA 19
|||
Db 21 LLAA 24

RESULT 33
Q62677
ID Q62677 PRELIMINARY; PRT; 28 AA.
AC Q62677; O09145; O09065;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alpha-1 collagen type IV (Fragment).
GN COL4A1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97107443; PubMed=8950183;
RA Grande J.P., Melder D.C., Kluge D.L., Wieben E.D.;
RT "Structure of the rat collagen IV promoter.";
RL Biochim. Biophys. Acta 1309:85-88(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Grande J.P., Haugen J.D.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U85606; AAB47426.1; -.
KW Collagen.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3113 MW; 96DFCAC741E07809 CRC64;

Query Match 10.3%; Score 4; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
||||
Db 13 LAAL 16

RESULT 34
Q8TGQ9
ID Q8TGQ9 PRELIMINARY; PRT; 29 AA.
AC Q8TGQ9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 3.3 kDa protein.
GN YNL103W-A.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21624570; PubMed=11753363;
RA Kumar A., Harrison P.M., Cheung K.H., Lan N., Echols N., Bertone P.,
RA Miller P., Gerstein M.B., Snyder M.;
RT "An integrated approach for finding overlooked genes in yeast.";
RL Nat. Biotechnol. 20:58-63(2002).
DR EMBL; AF479929; AAL79242.1; -.
KW Hypothetical protein.
SQ SEQUENCE 29 AA; 3350 MW; EC03E8528B54DF2E CRC64;

Query Match 10.3%; Score 4; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 KLLV 35
|||
Db 26 KLLV 29

RESULT 35

Q9BR24

ID Q9BR24 PRELIMINARY; PRT; 29 AA.
AC Q9BR24;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DJ269M15.2 (Protein tyrosine phosphatase, receptor type, T (RPTPRHO,
DE KIAA0283)) (Fragment).
GN PTPRT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL021395; CAC24740.2; -.
KW Receptor.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 2914 MW; AC6B6A4C94F4A38E CRC64;

Query Match 10.3%; Score 4; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 17 LAAL 20
|||
Db 4 LAAL 7

RESULT 36

Q9UBW6

ID Q9UBW6 PRELIMINARY; PRT; 29 AA.
AC Q9UBW6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE DR beta-3 protein (Fragment).
GN HLA-DRB3\$0201 OR HLA-DRB3\$0101 OR HLA-DRB3\$0301.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=93216303; PubMed=8462990;
RA Louis P., Eliaou J.F., Kerlan-Candon S., Pinet V., Vincent R.D.,

RA Clot J.;
RT "Polymorphism in the regulatory region of HLA-DRB genes correlating
RT with haplotype evolution.";
RL Immunogenetics 38:21-26(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Kerlan-Candon S.;
RL Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
DR EMBL; X65559; CAA46529.1; -.
DR EMBL; X65558; CAA46528.1; -.
DR EMBL; X65560; CAA46530.1; -.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 2951 MW; 2870A12FC80685DF CRC64;

Query Match 10.3%; Score 4; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
||||
Db 12 LAAL 15

RESULT 37

Q9UCW5
ID Q9UCW5 PRELIMINARY; PRT; 29 AA.
AC Q9UCW5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 11 beta-hydroxysteroid dehydrogenase type 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96064773; PubMed=7593417;
RA Wilson R.C., Harbison M.D., Krozowski Z.S., Funder J.W.,
RA Shackleton C.H., Hanuske-Abel H.M., Wei J.Q., Hertecant J., Moran A.,
RA Neiberger R.E.;
RT "Several homozygous mutations in the gene for 11 beta-hydroxysteroid
RT dehydrogenase type 2 in patients with apparent mineralocorticoid
RT excess.";
RL J. Clin. Endocrinol. Metab. 80:3145-3150(1995).
SQ SEQUENCE 29 AA; 3407 MW; CE826368D0714C00 CRC64;

Query Match 10.3%; Score 4; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAA 19
||||
Db 5 LLAA 8

RESULT 38

Q9BM71
ID Q9BM71 PRELIMINARY; PRT; 29 AA.
AC Q9BM71;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE LINE-like reverse transcriptase (Fragment).
OS Lasius niger.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Formicinae; Lasius.
OX NCBI_TaxID=67767;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=LRT-L1 retrotransposon;
RX MEDLINE=20570504; PubMed=11121049;
RA Arkhipova I., Meselson M.;
RT "Transposable elements in sexual and ancient asexual taxa.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14473-14477(2000).
DR EMBL; AY013922; AAG59907.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 1
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3060 MW; 6094F8E00837A336 CRC64;

Query Match 10.3%; Score 4; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LADD 7
||||
Db 18 LADD 21

RESULT 39
Q29891
ID Q29891 PRELIMINARY; PRT; 29 AA.
AC Q29891;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HLA-DRB protein (Fragment).
GN HLA-DRB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93216303; PubMed=8462990;
RA Louis P., Eliaou J.F., Kerlan-Candon S., Pinet V., Vincent R.D.,
RA Clot J.;
RT "Polymorphism in the regulatory region of the HLA-DRB genes
RT correlating with ancestral haplotype evolution.";
RL Immunogenetics 38:21-26(1993).
DR EMBL; X65585; CAA46544.1; -.
FT NON_TER 29 29

SQ SEQUENCE 29 AA; 2952 MW; 287F87E8CB7AF5DF CRC64;
Query Match 10.3%; Score 4; DB 7; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LALA 5
| || |
Db 26 LALA 29

RESULT 40

O19668

ID O19668 PRELIMINARY; PRT; 29 AA.
AC O19668;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HLA-DRB4\$0101 protein (Fragment).
GN HLA-DRB4\$0101.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Louis P.;
RL Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
DR EMBL; X65567; CAA46536.1; -.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 2862 MW; 2860BAE8CB6685DF CRC64;

Query Match 10.3%; Score 4; DB 7; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LALA 5
| || |
Db 26 LALA 29

Search completed: January 14, 2004, 10:42:28
Job time : 44.1589 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 6.43925 Seconds
(without alignments)
284.822 Million cell updates/sec

Title: US-09-843-221A-170

Perfect score: 39

Sequence: 1 SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP 39

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1319

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	%	Match	Length	DB	ID	Description
1	5	12.8	PETL_ARATH		31	1	PETL_ARATH	P56776	arabidopsis
2	5	12.8	PETL_BETVU		31	1	PETL_BETVU	P46612	beta vulgar
3	5	12.8	PETL_MAIZE		31	1	PETL_MAIZE	P19445	zea mays (m
4	5	12.8	PETL_OENHO		31	1	PETL_OENHO	Q9mtk4	oenothera h
5	5	12.8	PETL_ORYSA		31	1	PETL_ORYSA	P12180	oryza sativ
6	5	12.8	PETL_PGINU		31	1	PETL_PGINU	Q8wi03	psilotum nu
7	5	12.8	PETL_SPIOL		31	1	PETL_SPIOL	Q9m3l0	spinacia ol
8	5	12.8	PETL_TOBAC		31	1	PETL_TOBAC	P12181	nicotiana t
9	5	12.8	PETL_WHEAT		31	1	PETL_WHEAT	P58247	triticum ae
10	5	12.8	REV_SIVM2		37	1	REV_SIVM2	P08809	simian immu
11	4	10.3	PA22_MICNI		28	1	PA22_MICNI	P21791	micrurus ni
12	4	10.3	PETL_CYAPA		28	1	PETL_CYAPA	P48102	cyanophora
13	4	10.3	PETN_GUITH		29	1	PETN_GUITH	Q78498	guillardia
14	4	10.3	PETN_ODOSI		29	1	PETN_ODOSI	P49527	odontella s
15	4	10.3	PETN_SKECO		29	1	PETN_SKECO	O96807	skeletonema
16	4	10.3	PETN_CYACA		31	1	PETN_CYACA	Q9tlr6	cyanidium c
17	4	10.3	PSAM_CHLVU		31	1	PSAM_CHLVU	P56314	chlorella v

18	4	10.3	31	1	PSAM_SYN3	P72986 synechocyst
19	4	10.3	32	1	PSBZ_EUGST	Q8sl89 euglena ste
20	4	10.3	33	1	PBAN_LYMDI	P43511 lymantria d
21	4	10.3	33	1	YC12_MARPO	P31560 marchantia
22	4	10.3	35	1	PETG_CYACA	Q9tlq9 cyanidium c
23	4	10.3	36	1	PYY_RAJRH	P29206 raja rhina
24	4	10.3	37	1	DIU1_TENMO	P56618 tenebrio mo
25	4	10.3	37	1	RK36_NEPOL	Q9tl26 nephroselmi
26	4	10.3	38	1	CPRP_CANPG	P81033 cancer pagu
27	4	10.3	39	1	GVPC_SPICC	P81000 spirulina s
28	4	10.3	39	1	NPF_MONEX	P41967 moniezia ex
29	4	10.3	39	1	PHRI_BACSU	O31492 bacillus su
30	4	10.3	40	1	THIO_CLOSG	P81108 clostridium
31	4	10.3	40	1	UC11_MAIZE	P80617 zea mays (m
32	3	7.7	28	1	CH60_MYCSM	P80673 mycobacteri
33	3	7.7	28	1	MAAI_RAT	P57113 rattus norv
34	3	7.7	28	1	OBP1_HYSCR	P81647 hystrix cri
35	3	7.7	28	1	ORND_PLAOR	P25513 placobdella
36	3	7.7	28	1	SMS2_ORENI	P81029 oreochromis
37	3	7.7	28	1	VIP_ALLMI	P48142 alligator m
38	3	7.7	28	1	VIP_DIDMA	P39089 didelphis m
39	3	7.7	28	1	VIP_RANRI	P81016 rana ridibu
40	3	7.7	28	1	VIP_SCYCA	P09685 scyliorhinu
41	3	7.7	28	1	VIP_SHEEP	P04565 ovis aries
42	3	7.7	28	1	Y16P_BPT4	P39248 bacteriopha
43	3	7.7	29	1	ATP9_PICPJ	Q06838 pichia pip
44	3	7.7	29	1	ATPA_BRYMA	P26965 bryopsis ma
45	3	7.7	29	1	CERB_CERCA	P36191 ceratitis c
46	3	7.7	29	1	GALA_ALLMI	P47215 alligator m
47	3	7.7	29	1	GALA_AMICA	P47214 amia calva
48	3	7.7	29	1	GALA_CHICK	P30802 gallus gall
49	3	7.7	29	1	GALA_ONCMY	P47213 oncorhynchu
50	3	7.7	29	1	GALA_RANRI	P47216 rana ridibu
51	3	7.7	29	1	GALA_SHEEP	P31234 ovis aries
52	3	7.7	29	1	HOXY_RHOOP	P22660 rhodococcus
53	3	7.7	29	1	HS98_NEUCR	P31540 neurospora
54	3	7.7	29	1	KDPF_ECOLI	P36937 escherichia
55	3	7.7	29	1	PETN_ANASP	Q913p6 anabaena sp
56	3	7.7	29	1	PETN_ARATH	P12178 arabidopsis
57	3	7.7	29	1	PETN_CYAPA	P48258 cyanophora
58	3	7.7	29	1	PETN_MAIZE	Q33302 zea mays (m
59	3	7.7	29	1	PETN_MARPO	P12177 marchantia
60	3	7.7	29	1	PETN_PINTH	P41611 pinus thunb
61	3	7.7	29	1	PETN_PORPU	P51276 porphyra pu
62	3	7.7	29	1	PETN_PSINU	Q8wi23 psilotum nu
63	3	7.7	29	1	PETN_SYN3	P72717 synechocyst
64	3	7.7	29	1	PSAM_GUITH	O78448 guillardia
65	3	7.7	29	1	PSAX_SYN6	P23320 synechococc
66	3	7.7	29	1	RP54_CLOKL	P38944 clostridium
67	3	7.7	29	1	SODC_OLEEU	P80740 olea europa
68	3	7.7	29	1	TL16_SPIOL	P81834 spinacia ol
69	3	7.7	29	1	Y15_BPT7	P03792 bacteriopha
70	3	7.7	29	1	YCX_C_ODOSI	P49838 odontella s
71	3	7.7	30	1	AATC_RABIT	P12343 oryctolagus
72	3	7.7	30	1	CALM_LYTPI	P05935 lytechinus
73	3	7.7	30	1	CIRA_CHAPA	P56871 chassalia p
74	3	7.7	30	1	CY07_VIOOD	P58439 viola odora

75	3	7.7	30	1	DEF2_MACMU	P82317 macaca mula
76	3	7.7	30	1	DMS3_PHYSA	P80279 phyllomedus
77	3	7.7	30	1	FMBB_BACNO	P17829 bacteroides
78	3	7.7	30	1	HETA_RADMA	P58691 radianthus
79	3	7.7	30	1	ITI1_LAGLE	P26771 lagenaria l
80	3	7.7	30	1	ITR1_CITLIA	P11969 citrullus l
81	3	7.7	30	1	ITR1_MOMCH	P10294 momordica c
82	3	7.7	30	1	OTCC_AERPU	P11726 aeromonas p
83	3	7.7	30	1	PCG1_PACGO	P82414 pachycondyl
84	3	7.7	30	1	PCG2_PACGO	P82415 pachycondyl
85	3	7.7	30	1	PCG3_PACGO	P82416 pachycondyl
86	3	7.7	30	1	PMGY_CANAL	P82612 candida alb
87	3	7.7	30	1	PRT1_CLUPA	P02335 clupea pall
88	3	7.7	30	1	PSAM_MESVI	Q9mus2 mesostigma
89	3	7.7	30	1	PSAM_ODOSI	P49487 odontella s
90	3	7.7	30	1	RIPS_MOMCO	P20655 momordica c
91	3	7.7	30	1	RL18_HALCU	P05970 halobacteri
92	3	7.7	30	1	SDHA_CLOPR	P80212 clostridium
93	3	7.7	30	1	UP62_UPEIN	P82038 uperoleia i
94	3	7.7	30	1	URE1_ECOLI	Q03284 escherichia
95	3	7.7	30	1	VATN_BOVIN	P81134 bos taurus
96	3	7.7	30	1	VG03_BPPF1	P25137 bacteriopha
97	3	7.7	30	1	Y425_BORBU	O51386 borrelia bu
98	3	7.7	30	1	Y523_BORBU	O51473 borrelia bu
99	3	7.7	30	1	Y573_TREPA	O83583 treponema p
100	3	7.7	30	1	YCCB_ECOLI	P24244 escherichia
101	3	7.7	31	1	BCAM_PIG	O19098 sus scrofa
102	3	7.7	31	1	CTRP_PENMO	P35002 penaeus mon
103	3	7.7	31	1	CU54_LOCMI	P11738 locusta mig
104	3	7.7	31	1	DIUX_DIPPU	P82372 diptera
105	3	7.7	31	1	HBA_MACEU	P81043 macropus eu
106	3	7.7	31	1	HCY1_HOMAM	P82296 homarus ame
107	3	7.7	31	1	HCY2_MAISQ	P82303 maia squina
108	3	7.7	31	1	LPL_BUCRP	Q53017 buchnera ap
109	3	7.7	31	1	PETL_ANASP	Q8yvq2 anabaena sp
110	3	7.7	31	1	PETL_GUILTH	O78468 guillardia
111	3	7.7	31	1	PETL_LOTJA	Q9bbr4 lotus japon
112	3	7.7	31	1	PETL_MARPO	P12179 marchantia
113	3	7.7	31	1	PETL_MESVI	Q9mun4 mesostigma
114	3	7.7	31	1	PETL_NEPOL	Q9tky9 nephroselmi
115	3	7.7	31	1	PETL_ODOSI	P49524 odontella s
116	3	7.7	31	1	PETL_POPDE	O20272 populus del
117	3	7.7	31	1	PETM_CYACA	Q9tlr5 cyanidium c
118	3	7.7	31	1	PRT2_CLUPA	P02336 clupea pall
119	3	7.7	31	1	PSAM_CYAPA	P48185 cyanophora
120	3	7.7	31	1	PSAM_EUGGR	P31479 euglena gra
121	3	7.7	31	1	PSAM_SYNEL	P25903 synechococc
122	3	7.7	31	1	PSBK_SYNNU	P19054 synechococc
123	3	7.7	31	1	PSBM_MESVI	Q9muq7 mesostigma
124	3	7.7	31	1	PSBT_CHLRE	P37256 chlamydomon
125	3	7.7	31	1	PSBT_CHLVU	P56327 chlorella v
126	3	7.7	31	1	PSBT_CYAPA	P48109 cyanophora
127	3	7.7	31	1	PSBT_EUGGR	P20176 euglena gra
128	3	7.7	31	1	PSBT_MESVI	Q9muv6 mesostigma
129	3	7.7	31	1	PSBT_PORPU	P51323 porphyra pu
130	3	7.7	31	1	PYSG_METBA	P80523 methanosarc
131	3	7.7	31	1	RECX_METCL	P37865 methylomona

132	3	7.7	31	1	SARL_HUMAN	O00631 homo sapien
133	3	7.7	31	1	SARL_MOUSE	Q9cq6 mus musculu
134	3	7.7	31	1	SARL_RABIT	P42532 oryctolagus
135	3	7.7	31	1	Y3KD_BPCHP	P19187 bacteriopha
136	3	7.7	32	1	ADHR_DROYA	P28487 drosophila
137	3	7.7	32	1	APL3_DIAGR	P81471 diatraea gr
138	3	7.7	32	1	B4G1_RAT	P80225 r beta-1,4-
139	3	7.7	32	1	CAL2_ONCKE	P01264 oncorhynchus
140	3	7.7	32	1	CAL3_ONCKI	P01265 oncorhynchus
141	3	7.7	32	1	CAL_ANGJA	P01262 anguilla ja
142	3	7.7	32	1	CAPP_METEX	Q49136 methylobact
143	3	7.7	32	1	CYBL_RHOGR	P32953 rhodotorula
144	3	7.7	32	1	DBH_SYN1	P02343 synechocyst
145	3	7.7	32	1	FER_PORCR	P18821 porphyridiu
146	3	7.7	32	1	IAPP_SAGOE	Q28934 sanguinus oe
147	3	7.7	32	1	LPID_ECOLI	P03060 escherichia
148	3	7.7	32	1	LPID_EDWTA	P08140 edwardsiell
149	3	7.7	32	1	LPIV_ECOLI	P03061 escherichia
150	3	7.7	32	1	PETM_PORPU	P51275 porphyra pu
151	3	7.7	32	1	PRI3_ONCMY	P02330 oncorhynchus
152	3	7.7	32	1	PRT7_ONCMY	P08146 oncorhynchus
153	3	7.7	32	1	PRT8_ONCMY	P12817 oncorhynchus
154	3	7.7	32	1	PRT_ORYLA	Q91185 oryzias lat
155	3	7.7	32	1	PSAM_MARPO	P31590 marchantia
156	3	7.7	32	1	PSBQ_PEA	P19589 pisum sativ
157	3	7.7	32	1	PSBT_ODOSI	P49516 odontella s
158	3	7.7	32	1	PSBZ_EUGAN	Q8s195 euglena ana
159	3	7.7	32	1	PSBZ_EUGGA	Q8s193 euglena gra
160	3	7.7	32	1	PSBZ_EUGVI	Q8s187 euglena vir
161	3	7.7	32	1	Y160_BPT4	P39247 bacteriopha
162	3	7.7	32	1	Y433_BORB	O51394 borrelia bu
163	3	7.7	32	1	YCPG_MASLA	P29735 mastigoclad
164	3	7.7	32	1	YTK3_ILTVT	P23985 infectious
165	3	7.7	33	1	ALOX_PICPA	P04842 pichia past
166	3	7.7	33	1	ANP3_MYOSC	P04367 myoxocephal
167	3	7.7	33	1	ANP5_MYOAE	P20421 myoxocephal
168	3	7.7	33	1	DEF1_MESAU	P81465 mesocricetu
169	3	7.7	33	1	DEF3_MESAU	P81467 mesocricetu
170	3	7.7	33	1	FER_PORAE	P18820 porphyridiu
171	3	7.7	33	1	MBP1_MAIZE	P28794 zea mays (m
172	3	7.7	33	1	PETM_SYNEL	Q8dj15 synechococc
173	3	7.7	33	1	PK1_DICDI	P34101 dictyosteli
174	3	7.7	33	1	PRTB_MUGCE	P08130 mugil ceph
175	3	7.7	33	1	PRTL_ECOLI	P02338 escherichia
176	3	7.7	33	1	PSBT_ARATH	P37259 arabidopsis
177	3	7.7	33	1	PSBT_MAIZE	P37257 zea mays (m
178	3	7.7	33	1	RL4_HALCU	P05967 halobacteri
179	3	7.7	33	1	RPOC_HETCA	P36441 heterosigma
180	3	7.7	33	1	Y474_BORB	O51430 borrelia bu
181	3	7.7	33	1	Y50A_MYCTU	Q9cb56 mycobacteri
182	3	7.7	33	1	YC12_CHLRE	P50370 chlamydomon
183	3	7.7	33	1	YC12_MESVI	Q9mus3 mesostigma
184	3	7.7	34	1	COL_CHICK	P11148 gallus gall
185	3	7.7	34	1	COXA_THETH	P82543 thermus the
186	3	7.7	34	1	DEF2_RABIT	P07468 oryctolagus
187	3	7.7	34	1	DMS1_PHYSA	P24302 phyllomedus
188	3	7.7	34	1	DMS2_PHYSA	P80278 phyllomedus

189	3	7.7	34	1	HEMO_CHICK	P20057 gallus gall
190	3	7.7	34	1	MYTB_MYTED	P81613 mytilus edu
191	3	7.7	34	1	PETM_ANASP	Q9f4w2 anabaena sp
192	3	7.7	34	1	PRT1_SCOSC	P83264 scomber sco
193	3	7.7	34	1	PRT2_SCOSC	P83265 scomber sco
194	3	7.7	34	1	PRT_DICLA	Q9ps27 dicentrarch
195	3	7.7	34	1	PRT_PERFV	P29629 perca flave
196	3	7.7	34	1	PSBT_TOBAC	P12184 nicotiana t
197	3	7.7	34	1	PSPC_BOVIN	P15783 bos taurus
198	3	7.7	34	1	PSPC_CANFA	P22397 canis famil
199	3	7.7	34	1	RR2_OCHNE	Q40606 ochrosphaer
200	3	7.7	34	1	SMS_MYXGL	P19209 myxine glut
201	3	7.7	34	1	VLYS_BPM1	P08229 bacteriopha
202	3	7.7	34	1	VPU_HV1W2	P08808 human immun
203	3	7.7	34	1	Y870_HAEIN	P44065 haemophilus
204	3	7.7	34	1	YC12_GUITH	O78460 guillardia
205	3	7.7	34	1	YC12_ODOSI	P49529 odontella s
206	3	7.7	34	1	YC12_SKECO	O96797 skeletonema
207	3	7.7	35	1	ADO1_AGRDO	P58608 agriosphodr
208	3	7.7	35	1	ERFK_KLEAE	Q08599 klebsiella
209	3	7.7	35	1	EXE2_HELSU	P04204 heloderma s
210	3	7.7	35	1	NEF_HV1H3	P05854 human immun
211	3	7.7	35	1	PBP2_LYMDI	P34177 lymantria d
212	3	7.7	35	1	PSBT_MARPO	P12182 marchantia
213	3	7.7	35	1	PSBT_OENHO	P37258 oenothera h
214	3	7.7	35	1	PSBT_ORYSA	P12183 oryza sativ
215	3	7.7	35	1	PSBT_PINTH	P41625 pinus thunb
216	3	7.7	35	1	PSPC_PIG	P15785 sus scrofa
217	3	7.7	35	1	RL15_SYNTP7	P31160 synechococc
218	3	7.7	35	1	RL32_HALCU	P05965 halobacteri
219	3	7.7	35	1	SMS_LAMFL	Q9pr0 lampetra fl
220	3	7.7	35	1	TX1_THRPR	P83480 thrixopelma
221	3	7.7	35	1	WSP7_PINPS	P81086 pinus pinas
222	3	7.7	35	1	YC12_CYACA	Q9tlx0 cyanidium c
223	3	7.7	35	1	YQB5_CAEEL	Q09258 caenorhabdi
224	3	7.7	36	1	AMPL_PIG	P28839 sus scrofa
225	3	7.7	36	1	CECD_ANTPE	P01511 antheraea p
226	3	7.7	36	1	ELH_THETS	P80594 theromyzon
227	3	7.7	36	1	HBB_PONPY	Q9tt34 pongo pygma
228	3	7.7	36	1	LYOX_PIG	P45845 sus scrofa
229	3	7.7	36	1	MPG2_DACGL	Q41183 dactylis gl
230	3	7.7	36	1	MYPC_RAT	P56741 rattus norv
231	3	7.7	36	1	NEUH_CARCA	P11975 cardisoma c
232	3	7.7	36	1	NEUY_GADMO	P80167 gadus morhu
233	3	7.7	36	1	NEUY_ONCMY	P29071 oncorhynchus
234	3	7.7	36	1	NEUY_RABIT	P09640 oryctolagus
235	3	7.7	36	1	NEUY_RANRI	P29949 rana ridibu
236	3	7.7	36	1	NIFH_ENTAG	P26249 enterobacte
237	3	7.7	36	1	NUCM_SOLTU	P80264 solanum tub
238	3	7.7	36	1	OSTS YEAST	Q99380 saccharomyc
239	3	7.7	36	1	PAHO_ANSAN	P06304 anser anser
240	3	7.7	36	1	PAHO_DIDMA	P18107 didelphis m
241	3	7.7	36	1	PAHO_LARAR	P41337 larus argen
242	3	7.7	36	1	PAHO_RABIT	P41336 oryctolagus
243	3	7.7	36	1	PAHO_STRCA	P11967 struthio ca
244	3	7.7	36	1	PSAD_PEA	P20117 pisum sativ
245	3	7.7	36	1	PSAH_PEA	P20121 pisum sativ

246	3	7.7	36	1	PSAI_SKECO	O96813 skeletonema
247	3	7.7	36	1	PSBY_ODOSI	P49543 odontella s
248	3	7.7	36	1	PSBY_PORPU	P51206 porphyra pu
249	3	7.7	36	1	PYY_AMICA	P29205 amia calva
250	3	7.7	36	1	PYY_LEPSP	P09473 lepisosteus
251	3	7.7	36	1	PYY_ONCKI	P09474 oncorhynchus
252	3	7.7	36	1	R18A_BOVIN	P82919 bos taurus
253	3	7.7	36	1	Y297_ARCFU	O29945 archaeoglobus
254	3	7.7	36	1	Y699_TREPA	O83697 treponema p
255	3	7.7	36	1	YC12_CYAPA	P48256 cyanophora
256	3	7.7	37	1	24KD_PLACH	P14592 plasmodium
257	3	7.7	37	1	ANP3_PSEAM	P02733 pseudopleurus
258	3	7.7	37	1	CALR_RANRI	P31888 rana ridibunda
259	3	7.7	37	1	CEC2_MANSE	P14662 manduca sex
260	3	7.7	37	1	CEC3_MANSE	P14663 manduca sex
261	3	7.7	37	1	CEC4_MANSE	P14664 manduca sex
262	3	7.7	37	1	GHR3_RAT	P33580 rattus norvegicus
263	3	7.7	37	1	HCYB_CANPG	P83175 cancer pagurus
264	3	7.7	37	1	HOXF_RHOOP	P22658 rhodococcus
265	3	7.7	37	1	ME20_EUPRA	P26888 euplates ranae
266	3	7.7	37	1	OGT1_RABIT	P81436 oryctolagus
267	3	7.7	37	1	PETG_PORPU	P51318 porphyra pu
268	3	7.7	37	1	PETG_SKECO	O96811 skeletonema
269	3	7.7	37	1	PSBY_GUILTH	O78433 guillardia
270	3	7.7	37	1	PYY_CHICK	P29203 gallus gallus
271	3	7.7	37	1	RK36_ASTLO	P24355 astasia longa
272	3	7.7	37	1	RK36_EUGGR	P21532 euglena gracilis
273	3	7.7	37	1	RK36_PEA	P07815 pisum sativum
274	3	7.7	37	1	RK36_PORPU	P51296 porphyra pu
275	3	7.7	37	1	RL36_DEIRA	Q9rsk0 deinococcus
276	3	7.7	37	1	RL36_MYCLE	Q9x7a2 mycobacterium
277	3	7.7	37	1	RL36_MYCTU	P45810 mycobacterium
278	3	7.7	37	1	RL36_STRCO	O86772 streptomyces
279	3	7.7	37	1	RL36_THETH	P80256 thermus thermophilus
280	3	7.7	37	1	SMS_PETMA	P21779 petromyzon
281	3	7.7	37	1	TCTP_TRYBB	P35758 trypanosoma
282	3	7.7	37	1	THHS_HORVU	P33045 hordeum vulgare
283	3	7.7	37	1	VG65_BPPH2	P16515 bacteriophaga
284	3	7.7	37	1	VG65_BPPZA	P08384 bacteriophaga
285	3	7.7	37	1	VGJ_BPPHX	P03651 bacteriophaga
286	3	7.7	37	1	VPU_HV1Z8	P08807 human immunodeficiency virus
287	3	7.7	37	1	Y63_BPT3	P20328 bacteriophaga
288	3	7.7	37	1	YBGT_ECOLI	P56100 escherichia
289	3	7.7	37	1	YC12_CHLVU	P56328 chlorella vulgaris
290	3	7.7	37	1	YIM4_BPPH1	P10428 bacteriophaga
291	3	7.7	37	1	YRYL_CAEEL	Q19177 caenorhabditis elegans
292	3	7.7	38	1	EXE1_HELSU	P04203 heloderma suspectum
293	3	7.7	38	1	GME1_RAT	Q9quz8 rattus norvegicus
294	3	7.7	38	1	MUTS_YEREN	P47763 yersinia enterocolitica
295	3	7.7	38	1	NLT1_VITSX	P80275 vitis sp. (vitis vinifera)
296	3	7.7	38	1	NLT2_VITSX	P33556 vitis sp. (vitis labrusca)
297	3	7.7	38	1	PACA_URAJA	P81039 uranoscopus superciliosus
298	3	7.7	38	1	PSAI_ODOSI	P49484 odontella sphaerica
299	3	7.7	38	1	PSAI_SYNTP2	Q54752 synechococcus elongatus
300	3	7.7	38	1	PSBT_WHEAT	P37260 triticum aestivum
301	3	7.7	38	1	PSBX_ODOSI	P49509 odontella sphaericola
302	3	7.7	38	1	RL7_VIBCO	P05395 vibrio costatum

303	3	7.7	38	1	TRPD_SERMA	P12321 serratia ma
304	3	7.7	38	1	VCOM_BPD10	Q38200 bacteriopha
305	3	7.7	38	1	Y114_HAEIN	P43944 haemophilus
306	3	7.7	39	1	COL_SQUAC	P11149 squalus aca
307	3	7.7	39	1	FUC3_RAT	P80349 rattus norv
308	3	7.7	39	1	GDLO_DROME	Q9u5v6 drosophila
309	3	7.7	39	1	GLT2_WHEAT	P02862 triticum ae
310	3	7.7	39	1	H2A_BUFBG	P55897 bufo bufo g
311	3	7.7	39	1	LIMB_XENLA	P37138 xenopus lae
312	3	7.7	39	1	PHRF_BACSU	P71001 bacillus su
313	3	7.7	39	1	PRT1_BUFWA	P24641 bufo japoni
314	3	7.7	39	1	PRT2_BUFWA	P24642 bufo japoni
315	3	7.7	39	1	PSBI_SYN6	P17747 synechococc
316	3	7.7	39	1	PSBJ_GUITH	O78463 guillardia
317	3	7.7	39	1	PSBL_SYN3	Q55354 synechocyst
318	3	7.7	39	1	PSBX_CYAPA	P48266 cyanophora
319	3	7.7	39	1	PSBX_GUITH	O78455 guillardia
320	3	7.7	39	1	PSBX_PORPU	P51197 porphyra pu
321	3	7.7	39	1	PSI1_PSEFL	P80694 pseudomonas
322	3	7.7	39	1	SYS_RABIT	P13642 oryctolagus
323	3	7.7	39	1	VCOM_HAEIN	P71390 haemophilus
324	3	7.7	39	1	VLYS_BPOX2	P08230 bacteriopha
325	3	7.7	39	1	Y759_TREPA	O83740 treponema p
326	3	7.7	39	1	YU07_BORB	O54572 borrelia bu
327	3	7.7	40	1	ALB1_TRASC	P81188 trachemys s
328	3	7.7	40	1	ANP8_MYOAE	P20617 myoxocephal
329	3	7.7	40	1	CH60_SOLTU	P80502 solanum tub
330	3	7.7	40	1	EST4_DROMO	P10094 drosophila
331	3	7.7	40	1	GKBL_GINBI	P83171 ginkgo bilo
332	3	7.7	40	1	GP55_BPSP1	O48409 bacteriopha
333	3	7.7	40	1	HPT_RABIT	P19007 oryctolagus
334	3	7.7	40	1	PHAC_MASLA	P11389 mastigoclad
335	3	7.7	40	1	PHRC_BACSU	P94416 bacillus su
336	3	7.7	40	1	PHRK_BACSU	O31840 bacillus su
337	3	7.7	40	1	PSAI_PEA	P17227 pisum sativ
338	3	7.7	40	1	PSAJ_CYAPA	P48117 cyanophora
339	3	7.7	40	1	PSBJ_CYAPA	P19155 cyanophora
340	3	7.7	40	1	PTSA_LACLA	Q04938 lactococcus
341	3	7.7	40	1	RRPO_LSV	P27328 lily sympto
342	3	7.7	40	1	SAUV_PHYSA	P01144 phylomedus
343	3	7.7	40	1	Y41_BPT7	P03782 bacteriopha
344	3	7.7	40	1	YC04_ARCFU	O29064 archaeoglob
345	3	7.7	40	1	YC67_ARCFU	O29001 archaeoglob
346	3	7.7	40	1	YH76_ARCFU	O28498 archaeoglob
347	3	7.7	40	1	YSXC_SULAC	P39477 sulfolobus
348	2	5.1	28	1	ACON_CANAL	P82611 candida alb
349	2	5.1	28	1	APC1_RABIT	P33047 oryctolagus
350	2	5.1	28	1	ARYA_PSEPU	P35902 pseudomonas
351	2	5.1	28	1	ARYC_NOGL	P80008 nocardia gl
352	2	5.1	28	1	COXB_SOLTU	P80499 solanum tub
353	2	5.1	28	1	ETX2_BACCE	P80568 bacillus ce
354	2	5.1	28	1	FIBA_CANFA	P02673 canis famil
355	2	5.1	28	1	GDO_TRIMO	P02865 triticum mo
356	2	5.1	28	1	GRP_ALLMI	P31886 alligator m
357	2	5.1	28	1	GTS5_CHICK	P20137 gallus gall
358	2	5.1	28	1	GUN_SCHCO	P81190 schizophyll
359	2	5.1	28	1	GVPC_OSCAG	P80999 oscillatori

360	2	5.1	28	1	HORC_HORSP	P02864 hordeum spo
361	2	5.1	28	1	HSP4_OCTVU	P83216 octopus vul
362	2	5.1	28	1	ICPP_VIPLE	P82475 vipera lebe
363	2	5.1	28	1	IEL1_MOMCH	P10296 momordica c
364	2	5.1	28	1	IORB_METTM	P80911 methanobact
365	2	5.1	28	1	ITR3_LUFCY	P35628 luffa cylin
366	2	5.1	28	1	LECA_IRIHO	P36230 iris hollan
367	2	5.1	28	1	LPFS_ECOLI	P22183 escherichia
368	2	5.1	28	1	LPL_ECOLI	P09149 escherichia
369	2	5.1	28	1	LPL_SALTI	Q8z9h9 salmonella
370	2	5.1	28	1	LPL_SALTY	P03062 salmonella
371	2	5.1	28	1	LPW_SERMA	P03055 serratia ma
372	2	5.1	28	1	MT2_BRANA	Q96353 brassica na
373	2	5.1	28	1	NLT2_WHEAT	P39085 triticum ae
374	2	5.1	28	1	OMPA_YERPS	P38399 yersinia ps
375	2	5.1	28	1	OST1_CHICK	P80896 gallus gall
376	2	5.1	28	1	PA23_TRIST	P82894 trimeresuru
377	2	5.1	28	1	PHR_METTM	P58818 methanobact
378	2	5.1	28	1	PHYB_ASPIFI	P81440 aspergillus
379	2	5.1	28	1	PP71_HCMVT	P24429 human cytom
380	2	5.1	28	1	PPOX_BOVIN	P56602 bos taurus
381	2	5.1	28	1	RIP_PLETU	P83245 pleurotus t
382	2	5.1	28	1	RL5_HALCU	P05972 halobacteri
383	2	5.1	28	1	RS19_PHYS1	O66093 phytoplasma
384	2	5.1	28	1	SCX2_BUTSI	P15230 buthus sind
385	2	5.1	28	1	SLP1_LEIQH	P80669 leiurus qui
386	2	5.1	28	1	TXO2_AGEAP	P15971 agelenopsis
387	2	5.1	28	1	UC05_MAIZE	P80611 zea mays (m
388	2	5.1	28	1	VAO_PLEOS	P21800 pleurotus o
389	2	5.1	28	1	VG9_SPV4	P11341 spiroplasma
390	2	5.1	28	1	VI03_VACCP	Q00334 vaccinia vi
391	2	5.1	28	1	Y073_ARCFU	O30163 archaeoglob
392	2	5.1	28	1	YA79_ARCFU	O29184 archaeoglob
393	2	5.1	29	1	28KD_TRIFO	P33405 tritrichomo
394	2	5.1	29	1	AL21_HORSE	P81216 equus cabal
395	2	5.1	29	1	AMEL_RABIT	P12761 oryctolagus
396	2	5.1	29	1	BR2D_RANES	P40840 rana escule
397	2	5.1	29	1	BREE_RANES	P40841 rana escule
398	2	5.1	29	1	COA1_BPI22	P15413 bacteriopha
399	2	5.1	29	1	COXJ_CANFA	Q9tr29 canis famil
400	2	5.1	29	1	COXK_SHEEP	Q9tr28 ovis aries
401	2	5.1	29	1	CU36_LOCMI	P11737 locusta mig
402	2	5.1	29	1	CXD6_CONGL	Q9twm7 conus glori
403	2	5.1	29	1	CXO7_CONGE	P05483 conus geogr
404	2	5.1	29	1	CXOC_CONMA	P37300 conus magus
405	2	5.1	29	1	DMD_RAT	P11530 rattus norv
406	2	5.1	29	1	DMS5_PHYSA	P80281 phylomedus
407	2	5.1	29	1	GLUC_ANAPL	P01276 anas platyr
408	2	5.1	29	1	GLUC_CALMI	P13189 callorhynch
409	2	5.1	29	1	GLUC_CHIBR	P31297 chinchilla
410	2	5.1	29	1	GLUC_DIDMA	P18108 didelphis m
411	2	5.1	29	1	GLUC_LAMFL	Q9prq9 lampetra fl
412	2	5.1	29	1	GLUC_PLAFE	P23062 platichthys
413	2	5.1	29	1	GLUC_RABIT	P25449 oryctolagus
414	2	5.1	29	1	GLUC_TORMA	P09567 torpedo mar
415	2	5.1	29	1	H2B2_ECHES	P13282 echinus esc
416	2	5.1	29	1	HRJ_BOTJA	P20416 bothrops ja

417	2	5.1	29	1	I PYR DESVH	P19371 desulfovibr
418	2	5.1	29	1	I TH3 BOVIN	P56652 bos taurus
419	2	5.1	29	1	I TR1 CUCMA	P01074 cucurbita m
420	2	5.1	29	1	I TR1 LUF CY	P25849 luffa cylin
421	2	5.1	29	1	I TR1 MOMRE	P17680 momordica r
422	2	5.1	29	1	I TR2 BRYDI	P11968 bryonia dio
423	2	5.1	29	1	I TR3 CYCPE	P83394 cyclanthera
424	2	5.1	29	1	I TR4 CYCPE	P83395 cyclanthera
425	2	5.1	29	1	I TR5 CYCPE	P83396 cyclanthera
426	2	5.1	29	1	M DH BURPS	P80536 burkholderi
427	2	5.1	29	1	MUL R ECHML	P81798 echis multi
428	2	5.1	29	1	N NUO1 SOLTU	P80267 solanum tub
429	2	5.1	29	1	P2SM LOXIN	P83046 loxosceles
430	2	5.1	29	1	PCG4 PACGO	P82417 pachycondyl
431	2	5.1	29	1	PETN CHAGL	Q8ma13 chaetosphae
432	2	5.1	29	1	PETN MESVI	Q9mus4 mesostigma
433	2	5.1	29	1	PETN SYNEL	Q8dkn2 synechococc
434	2	5.1	29	1	PK4 DICDI	P34103 dictyosteli
435	2	5.1	29	1	PRO1 DACGL	P18689 dactylis gl
436	2	5.1	29	1	PSAF SYN P6	P31083 synechococc
437	2	5.1	29	1	PSBI SYNVU	P12240 synechococc
438	2	5.1	29	1	RL15 HALCU	P05971 halobacteri
439	2	5.1	29	1	RL15 STRLI	P49975 streptomyce
440	2	5.1	29	1	RS7 METTE	O93639 methanosarc
441	2	5.1	29	1	SLP2 LEIQH	P80670 leiurus qui
442	2	5.1	29	1	SLP3 LEIQH	P80671 leiurus qui
443	2	5.1	29	1	TLP ACTDE	P81370 actinidia d
444	2	5.1	29	1	UN23 CLOPA	P81356 clostridium
445	2	5.1	29	1	Y51 BPT3	P20326 bacteriopha
446	2	5.1	29	1	YCX4 ODOSI	P49830 odontella s
447	2	5.1	30	1	2ENR CLOTY	P11887 clostridium
448	2	5.1	30	1	A1AT CHIVI	P38026 chinchilla
449	2	5.1	30	1	AATM RABIT	P12345 oryctolagus
450	2	5.1	30	1	ACB1 DIGLA	P81624 digitalis l
451	2	5.1	30	1	AMPT BACST	P00728 bacillus st
452	2	5.1	30	1	ANF RANRI	P09196 rana ridibu
453	2	5.1	30	1	CBAL BACST	P13722 bacillus st
454	2	5.1	30	1	CH60 CLOPA	P81339 clostridium
455	2	5.1	30	1	CLPA PINPS	P81671 pinus pinas
456	2	5.1	30	1	COAE CORAM	P58101 corynebacte
457	2	5.1	30	1	COXC SOLTU	P80500 solanum tub
458	2	5.1	30	1	CX2A CONBE	P58625 conus betul
459	2	5.1	30	1	CXEX CONCN	P58928 conus conso
460	2	5.1	30	1	CXK4 CONST	P58921 conus stria
461	2	5.1	30	1	CXOB CONPE	P56713 conus penna
462	2	5.1	30	1	CXVA CONER	P58782 conus ermin
463	2	5.1	30	1	CXVB CONER	P58783 conus ermin
464	2	5.1	30	1	CY35 DESAC	P81079 desulfuromo
465	2	5.1	30	1	CYO1 VIOOD	P82230 viola odora
466	2	5.1	30	1	DIDH COMTE	P80702 comamonas t
467	2	5.1	30	1	DIU2 HYLLI	P82015 hyles linea
468	2	5.1	30	1	DIU2 MANSE	P24858 manduca sex
469	2	5.1	30	1	END2 ONCKE	P01205 oncorhynchus
470	2	5.1	30	1	FIBR PANIN	P22775 panulirus i
471	2	5.1	30	1	FTN BACFR	P28733 bacteroides
472	2	5.1	30	1	GLUM ANGAN	P41521 anguilla an
473	2	5.1	30	1	HCY2 HOMAM	P82297 homarus ame

474	2	5.1	30	1	HSP5_OCTVU	P83217 octopus vul
475	2	5.1	30	1	HYPA_HYBPA	P58445 hybanthus p
476	2	5.1	30	1	IHFBI_RHILE	P80606 rhizobium l
477	2	5.1	30	1	ITR2_ECBEL	P12071 ecballium e
478	2	5.1	30	1	ITR2_LUFCY	P25850 luffa cylin
479	2	5.1	30	1	ITR3_CUCMC	P32041 cucumis mel
480	2	5.1	30	1	ITR3_MOMCO	P82410 momordica c
481	2	5.1	30	1	ITR4_CUCSA	P10292 cucumis sat
482	2	5.1	30	1	ITR6_CYCPE	P83397 cyclanthera
483	2	5.1	30	1	ITR7_CYCPE	P83398 cyclanthera
484	2	5.1	30	1	KAB5_OLDAF	P58456 oldenlandia
485	2	5.1	30	1	LAS1_PIG	P80171 sus scrofa
486	2	5.1	30	1	LEAH_PHAVU	P81870 phaseolus v
487	2	5.1	30	1	MDH_HELGE	P80037 heliobacter
488	2	5.1	30	1	MMAL_DERMI	P16312 dermatophag
489	2	5.1	30	1	NU5M_PISOC	P24999 pisaster oc
490	2	5.1	30	1	NUO2_SOLTU	P80268 solanum tub
491	2	5.1	30	1	P2CO_ARTSP	P37365 arthrobacte
492	2	5.1	30	1	PCCA_MYXXA	P81185 myxococcus
493	2	5.1	30	1	PCG5_PACGO	P82418 pachycondyl
494	2	5.1	30	1	PETN_NEPOL	Q9t101 nephroselmi
495	2	5.1	30	1	PLF4_RABIT	P83470 oryctolagus
496	2	5.1	30	1	PLMS_SQUAC	P82542 squalus aca
497	2	5.1	30	1	PRT2_ONCMY	P02331 oncorhynchu
498	2	5.1	30	1	PRT3_ONCMY	P02332 oncorhynchu
499	2	5.1	30	1	PRT4_ONCMY	P02333 oncorhynchu
500	2	5.1	30	1	PRTB_ONCMY	P12819 oncorhynchu
501	2	5.1	30	1	PSAM_CYACA	Q9t1x5 cyanidium c
502	2	5.1	30	1	PSAM_PINTH	P41601 pinus thunb
503	2	5.1	30	1	PSAM_PORPU	P51395 porphyra pu
504	2	5.1	30	1	PYSD_METBA	P80524 methanosarc
505	2	5.1	30	1	RKGG_LEPKE	P21587 lepidochely
506	2	5.1	30	1	RNP_ODOVI	P19640 odocoileus
507	2	5.1	30	1	SCK2_TITSE	P08816 tityus serr
508	2	5.1	30	1	SCX2_CENLI	P18927 centruroides
509	2	5.1	30	1	SILU_RHIPU	P02885 rhizomucor
510	2	5.1	30	1	TL29_SPIOL	P81833 spinacia ol
511	2	5.1	30	1	TX2_HETVE	P58426 heteropoda
512	2	5.1	30	1	TX2_THRPR	P83476 thrixopelma
513	2	5.1	30	1	UC35_MAIZE	P80641 zea mays (m)
514	2	5.1	30	1	UDDP_SULAC	P80143 sulfolobus
515	2	5.1	30	1	UP61_UPEIN	P82037 uperoleia i
516	2	5.1	30	1	VAA1_EQUAR	Q04236 equisetum a
517	2	5.1	30	1	VAA1_PSINU	Q04237 psilotum nu
518	2	5.1	30	1	VAA2_EQUAR	Q04238 equisetum a
519	2	5.1	30	1	VAA2_PSINU	Q04239 psilotum nu
520	2	5.1	30	1	VPU_HV1SC	P05948 human immun
521	2	5.1	30	1	VTTA_BPT3	P20837 bacteriopha
522	2	5.1	30	1	Y161_TREPA	O83196 treponema p
523	2	5.1	30	1	Y357_BORBU	O51332 borrelia bu
524	2	5.1	30	1	Y932_TREPA	O83902 treponema p
525	2	5.1	31	1	A98A_DROME	O46201 drosophila
526	2	5.1	31	1	ANP3_PAGBO	P02732 pagothenia
527	2	5.1	31	1	CEC1_PIG	P14661 sus scrofa
528	2	5.1	31	1	CIRB_CHAPA	P56879 chassalia p
529	2	5.1	31	1	COG5_BOVIN	P83437 bos taurus
530	2	5.1	31	1	COX4_NEUCR	P06809 neurospora

531	2	5.1	31	1	CTX2_CORVA	P82601 coremiocnem
532	2	5.1	31	1	CXD6_CONNI	P56710 conus nigro
533	2	5.1	31	1	CXG6_CONTE	P58922 conus texti
534	2	5.1	31	1	CXOA_CONPE	P56712 conus penna
535	2	5.1	31	1	CYLA_PSYLO	P56872 psychotria
536	2	5.1	31	1	CYO6_VIOOD	P58438 viola odora
537	2	5.1	31	1	DEF2_MESAU	P81466 mesocricetu
538	2	5.1	31	1	DEJP_DROME	P81160 drosophila
539	2	5.1	31	1	EFTU_STRLU	P52390 streptomyce
540	2	5.1	31	1	ENDB_CAMDR	P01203 camelus dro
541	2	5.1	31	1	ER29_BOVIN	P81623 bos taurus
542	2	5.1	31	1	ETFD_PARDE	P55932 paracoccus
543	2	5.1	31	1	FIBB_CANFA	P02677 canis famil
544	2	5.1	31	1	GP37_BPSP1	O48393 bacteriopha
545	2	5.1	31	1	GT_SERMA	P22416 serratia ma
546	2	5.1	31	1	GUN2_SCLSC	P21834 sclerotinia
547	2	5.1	31	1	H13_WHEAT	P15872 triticum ae
548	2	5.1	31	1	HEM2_PHAGO	P27687 phascolopsi
549	2	5.1	31	1	KLK1_CAVPO	P12322 cavia porce
550	2	5.1	31	1	LC70_LACPA	P80959 lactobacill
551	2	5.1	31	1	LCCB_LEUME	P81052 leuconostoc
552	2	5.1	31	1	LPRM_ECOLI	P10739 escherichia
553	2	5.1	31	1	MALK_PHOLU	P41124 photorhabdu
554	2	5.1	31	1	MDH_STRAR	P19982 streptomyce
555	2	5.1	31	1	NAP4_HUMAN	P19877 homo sapien
556	2	5.1	31	1	PETL_CHLVU	P56306 chlorella v
557	2	5.1	31	1	PETL_PORPU	P51221 porphyra pu
558	2	5.1	31	1	PRT3_CLUPA	P02337 clupea pall
559	2	5.1	31	1	PSAK_ANAVA	P23317 anabaena va
560	2	5.1	31	1	SC37_MESMA	P83407 mesobuthus
561	2	5.1	31	1	SCK5_ANDMA	P31719 androctonus
562	2	5.1	31	1	SCKL_LEIQH	P16341 leiurus qui
563	2	5.1	31	1	SODC_STRHE	P81163 striga herm
564	2	5.1	31	1	TX3_HETVE	P58427 heteropoda
565	2	5.1	31	1	Y603_ARCFU	O29652 archaeoglob
566	2	5.1	31	1	Y822_BORB	O51762 borrelia bu
567	2	5.1	32	1	A2M_PACLE	P20738 pacifastacu
568	2	5.1	32	1	ATP0_PIG	P80021 sus scrofa
569	2	5.1	32	1	ATP7_SPIOL	P80088 spinacia ol
570	2	5.1	32	1	ATPO_SPIOL	P80087 spinacia ol
571	2	5.1	32	1	CAAP_MICEC	P21162 micromonosp
572	2	5.1	32	1	CALO_BOVIN	P01260 bos taurus
573	2	5.1	32	1	CALO_PIG	P01259 sus scrofa
574	2	5.1	32	1	CAR1_ECHCA	Q9prp9 echis carin
575	2	5.1	32	1	CEC_OIKKI	P83420 oiketicus k
576	2	5.1	32	1	COA1_BPIF1	O80295 bacteriopha
577	2	5.1	32	1	COA1_BPIKE	P03676 bacteriopha
578	2	5.1	32	1	COA2_BPFD	P03677 bacteriopha
579	2	5.1	32	1	COA2_BPIF1	O80296 bacteriopha
580	2	5.1	32	1	CRP_PLEPL	P12245 pleuronecte
581	2	5.1	32	1	CXG7_CONPE	P56711 conus penna
582	2	5.1	32	1	CY31_DESAC	P81078 desulfuromo
583	2	5.1	32	1	CYSB_FASHE	P80529 fasciola he
584	2	5.1	32	1	ER29_CHICK	P81628 gallus gall
585	2	5.1	32	1	ER29_TRIVU	P81629 trichosurus
586	2	5.1	32	1	ERH_PIG	P80230 sus scrofa
587	2	5.1	32	1	FF21_SALEN	P55224 salmonella

588	2	5.1	32	1	FLA1_METHU	P17603 methanospir
589	2	5.1	32	1	FRIH_ANAPL	P80145 anas platyr
590	2	5.1	32	1	GHR4_RAT	P33581 rattus norv
591	2	5.1	32	1	GLB4_LAMSP	P20413 lamellibrac
592	2	5.1	32	1	GT82_DICL8	P82608 dicentrarch
593	2	5.1	32	1	H2AZ_ONCMY	P22647 oncorhynchus
594	2	5.1	32	1	HCYC_CHEDE	P83172 cherax dest
595	2	5.1	32	1	IAPP_BOVIN	Q28207 bos taurus
596	2	5.1	32	1	IAPP_PIG	Q29119 sus scrofa
597	2	5.1	32	1	IAPP_SHEEP	Q28605 ovis aries
598	2	5.1	32	1	ILVB_ENTAE	Q09129 enterobacte
599	2	5.1	32	1	ITR2_CUCSA	P10291 cucumis sat
600	2	5.1	32	1	ITR3_CUCPE	P10293 cucurbita p
601	2	5.1	32	1	ITR4_CUCMA	P07853 cucurbita m
602	2	5.1	32	1	LEC_DOLAX	P02875 dolichos ax
603	2	5.1	32	1	MDH_NITAL	P10887 nitzschia a
604	2	5.1	32	1	MIFH_TRITR	P81748 trichuris t
605	2	5.1	32	1	NEUB_PIG	P01297 sus scrofa
606	2	5.1	32	1	OVOS_ANAPL	P20739 anas platyr
607	2	5.1	32	1	P1SM_LOXIN	P83045 loxosceles
608	2	5.1	32	1	PA22_AGKHP	P18997 agkistrodon
609	2	5.1	32	1	PA2_RHONO	P43318 rhopilema n
610	2	5.1	32	1	PETL_CHLRE	P50369 chlamydomon
611	2	5.1	32	1	PETM_GUITH	O78499 guillardia
612	2	5.1	32	1	PHNS_DESMU	P13062 desulfovibr
613	2	5.1	32	1	PHSS_DESBN	P13064 desulfovibr
614	2	5.1	32	1	PRT1_ESOLU	P02325 esox lucius
615	2	5.1	32	1	PRT1_ONCKE	P02327 oncorhynchus
616	2	5.1	32	1	PRT4_SCYCA	P30259 scyliorhinus
617	2	5.1	32	1	PRT5_ONCMY	P02334 oncorhynchus
618	2	5.1	32	1	PRT6_ONCMY	P08145 oncorhynchus
619	2	5.1	32	1	PRT9_ONCMY	P08147 oncorhynchus
620	2	5.1	32	1	PRTA_ONCMY	P12818 oncorhynchus
621	2	5.1	32	1	PRTE_HALME	P28308 halobacteri
622	2	5.1	32	1	PSBT_CYACA	O19927 cyanidium c
623	2	5.1	32	1	PSBT_GUITH	O78512 guillardia
624	2	5.1	32	1	PSBZ_EUGMY	Q8s191 euglena myx
625	2	5.1	32	1	RIP2_PHYDI	P34967 phytolacca
626	2	5.1	32	1	RK1_RABIT	P81655 oryctolagus
627	2	5.1	32	1	RS19_YEREN	Q56847 yersinia en
628	2	5.1	32	1	TAT_SIVM2	P05912 simian immu
629	2	5.1	32	1	TX29_PHONI	P29426 phoneutria
630	2	5.1	32	1	TXP7_APTSC	P49271 aptostichus
631	2	5.1	32	1	UC09_MAIZE	P80615 zea mays (m
632	2	5.1	32	1	Y169_TREPA	O83199 treponema p
633	2	5.1	32	1	YH17_HAEIN	P44295 haemophilus
634	2	5.1	32	1	YL55_CAEEL	P34435 caenorhabdi
635	2	5.1	32	1	YSCA_YEREN	Q01242 yersinia en
636	2	5.1	33	1	ACT_DICVI	Q24733 dictyocaulu
637	2	5.1	33	1	ATP7_SOLTU	P80496 solanum tub
638	2	5.1	33	1	BR2A_RANES	P40837 rana escule
639	2	5.1	33	1	BR2B_RANES	P40838 rana escule
640	2	5.1	33	1	BR2E_RANES	P32413 rana escule
641	2	5.1	33	1	BR2_RANBP	P32424 rana brevip
642	2	5.1	33	1	CECB_HELVI	P83414 heliothis v
643	2	5.1	33	1	CECC_HELVI	P83415 heliothis v
644	2	5.1	33	1	COA1_BPFD	P03675 bacteriopha

645	2	5.1	33	1	COA2_BPI22	P15414 bacteriopha
646	2	5.1	33	1	COA2_BPIKE	P03678 bacteriopha
647	2	5.1	33	1	COXL_ONCMY	P80330 oncorhynchus
648	2	5.1	33	1	CU89_HUMAN	P59042 homo sapien
649	2	5.1	33	1	CXO_CONVE	P83301 conus ventr
650	2	5.1	33	1	DBB2_DOLAU	P83376 dolabella a
651	2	5.1	33	1	DEF4_MESAU	P81468 mesocricetus
652	2	5.1	33	1	DHE3_PIG	P42174 sus scrofa
653	2	5.1	33	1	FABI_RHASA	P81175 rhamdia sap
654	2	5.1	33	1	GAST_CAVPO	P06885 cavia porcellus
655	2	5.1	33	1	GAST_CHIBR	P10034 chinchilla
656	2	5.1	33	1	GAST_DIDMA	P33713 didelphis marsupialis
657	2	5.1	33	1	GGN1_RANRU	P80395 rana rugosa
658	2	5.1	33	1	GGN2_RANRU	P80396 rana rugosa
659	2	5.1	33	1	GGN3_RANRU	P80397 rana rugosa
660	2	5.1	33	1	GLU2_ORENI	P81027 oreochromis
661	2	5.1	33	1	HF40_MAIZE	P82865 zea mays (m)
662	2	5.1	33	1	HOXU_RHOOP	P22659 rhodococcus
663	2	5.1	33	1	LPPY_SALTY	P08522 salmonella
664	2	5.1	33	1	LPRH_ECOLI	P37324 escherichia
665	2	5.1	33	1	LYC2_HORSE	P81710 equus caballus
666	2	5.1	33	1	MHAA_STRCH	P80435 streptomyces
667	2	5.1	33	1	MYMY_MYTED	P81614 mytilus edulis
668	2	5.1	33	1	OREX_BOVIN	P56717 bos taurus
669	2	5.1	33	1	OTCC_PSEPU	P11727 pseudomonas
670	2	5.1	33	1	PAP1_PARPV	P81865 pardachirus
671	2	5.1	33	1	PAP2_PARPV	P23067 pardachirus
672	2	5.1	33	1	PAP3_PARPV	P81866 pardachirus
673	2	5.1	33	1	PAP4_PARMA	P81861 pardachirus
674	2	5.1	33	1	PAP5_PARMA	P81862 pardachirus
675	2	5.1	33	1	PEN3_ADECU	P35987 canine adenovirus
676	2	5.1	33	1	PETM_CYAPA	P48366 cyanophora
677	2	5.1	33	1	PK5_DICDI	P34104 dictyostelia
678	2	5.1	33	1	PRI1_ONCMY	P02326 oncorhynchus
679	2	5.1	33	1	PRI2_ONCMY	P02328 oncorhynchus
680	2	5.1	33	1	PSAI_SPIOL	P17228 spinacia oliveriana
681	2	5.1	33	1	PSAK_CUCSA	P42051 cucumis sativus
682	2	5.1	33	1	RL21_XENLA	P49628 xenopus laevis
683	2	5.1	33	1	RL26_XENLA	P49629 xenopus laevis
684	2	5.1	33	1	RL28_XENLA	P46780 xenopus laevis
685	2	5.1	33	1	RRPO_BPZ1	P09674 bacteriopha
686	2	5.1	33	1	RS4_XENLA	P49401 xenopus laevis
687	2	5.1	33	1	RT25_BOVIN	P82669 bos taurus
688	2	5.1	33	1	RUGA_RANRU	P80954 rana rugosa
689	2	5.1	33	1	RUGB_RANRU	P80955 rana rugosa
690	2	5.1	33	1	SC63_CANFA	P82008 canis familiaris
691	2	5.1	33	1	SCX9_BUTOC	P04099 buthus occidentalis
692	2	5.1	33	1	T1F_PARTE	Q27172 paramecium
693	2	5.1	33	1	THIO_CLOST	P81109 clostridium
694	2	5.1	33	1	TXH1_SELHU	P56676 selenocosmus
695	2	5.1	33	1	TXN3_SELHA	P83464 selenocosmus
696	2	5.1	33	1	VT1B_RAT	P58200 rattus norvegicus
697	2	5.1	33	1	Y849_BORBU	O51789 borrelia burgdorferi
698	2	5.1	33	1	YC12_EUGGR	P31559 euglena gracilis
699	2	5.1	33	1	YC12_NEPOL	Q9tky6 nephrosermi
700	2	5.1	33	1	YC12_PINTH	P41600 pinus thunbergii
701	2	5.1	33	1	YL74_ARCFU	O28108 archaeoglobus

702	2	5.1	33	1	YLCH_BP82	Q37869 bacteriopha
703	2	5.1	33	1	YLCH_ECOLI	Q47268 escherichia
704	2	5.1	34	1	AMP2_CHICK	P80390 gallus gall
705	2	5.1	34	1	ASPG_PIG	P30918 sus scrofa
706	2	5.1	34	1	BR2C_RANES	P40839 rana escule
707	2	5.1	34	1	BUTH_ANDAU	P56685 androctonus
708	2	5.1	34	1	COXG_THUOB	P80976 thunnus obe
709	2	5.1	34	1	DEF7_RABIT	P80223 oryctolagus
710	2	5.1	34	1	ECAB_ECTTU	P49344 ectatomma t
711	2	5.1	34	1	EF2_RABIT	P55823 oryctolagus
712	2	5.1	34	1	EGGR_APLCA	P01363 aplysia cal
713	2	5.1	34	1	EM1_ENSMI	P27205 ensis minor
714	2	5.1	34	1	GAST_CAPHI	P04564 capra hircu
715	2	5.1	34	1	GUN1_SCLSC	P21833 sclerotinia
716	2	5.1	34	1	H1S_STRPU	P19376 strongyloce
717	2	5.1	34	1	HS7S_CUCMA	P31082 cucurbita m
718	2	5.1	34	1	ITR1_MOMCO	P82408 momordica c
719	2	5.1	34	1	ITR2_MOMCO	P82409 momordica c
720	2	5.1	34	1	LPTN_PROVU	P28779 proteus vul
721	2	5.1	34	1	M44E_HUMAN	Q96pg1 homo sapien
722	2	5.1	34	1	MYTA_MYTED	P81612 mytilus edu
723	2	5.1	34	1	PRT1_SAROR	P25327 sarda orien
724	2	5.1	34	1	PRT1_THUTH	P02321 thunnus thy
725	2	5.1	34	1	PRT2_THUTH	P02322 thunnus thy
726	2	5.1	34	1	PSAI_LOTJA	Q9bbs0 lotus japon
727	2	5.1	34	1	PSAI_OENHO	Q9mtl2 oenothera h
728	2	5.1	34	1	PSAI_SOYBN	P49159 glycine max
729	2	5.1	34	1	PSBM_ARATH	P12169 arabidopsis
730	2	5.1	34	1	PSBM_CHAGL	Q8ma15 chaetosphae
731	2	5.1	34	1	PSBM_CHLRE	P92277 chlamydomon
732	2	5.1	34	1	PSBM_MAIZE	P48189 zea mays (m
733	2	5.1	34	1	PSBM_MARPO	P12168 marchantia
734	2	5.1	34	1	PSBM_NEPOL	Q9tl37 nephroselmi
735	2	5.1	34	1	PSBM_OENHO	Q9mtm8 oenothera h
736	2	5.1	34	1	PSBM_PEA	P34833 pisum sativ
737	2	5.1	34	1	PSBM_PSINU	Q8wi22 psilotum nu
738	2	5.1	34	1	PSBM_WHEAT	Q9xps6 triticum ae
739	2	5.1	34	1	PTU1_PEITU	P58606 peirates tu
740	2	5.1	34	1	PYSB_METBA	P80522 methanosarc
741	2	5.1	34	1	RNL1_PIG	P15466 sus scrofa
742	2	5.1	34	1	SCXM_SCOMA	P80719 scorpio mau
743	2	5.1	34	1	THEM_MALSU	P13858 malbranchea
744	2	5.1	34	1	TX1_SCogr	P56855 scodra gris
745	2	5.1	34	1	TXP5_BRASM	P49266 brachypelma
746	2	5.1	34	1	Y05J_BPT4	P39239 bacteriopha
747	2	5.1	34	1	Y224_TREPA	O83253 treponema p
748	2	5.1	34	1	Y848_BORBUT	O51788 borrelia bu
749	2	5.1	34	1	Y967_HAEIN	P44086 haemophilus
750	2	5.1	34	1	YC12_PORPU	P51385 porphyra pu
751	2	5.1	34	1	YMIA_AGRTU	P38437 agrobacteri
752	2	5.1	35	1	C550_BACHA	P80091 bacillus ha
753	2	5.1	35	1	CEC4_BOMMO	P14666 bombyx mori
754	2	5.1	35	1	CECA_AEDAL	P81417 aedes albop
755	2	5.1	35	1	CECA_HELVI	P83413 heliothis v
756	2	5.1	35	1	CECB_ANTPE	P01509 antheraea p
757	2	5.1	35	1	CHI1_CASSA	P29137 castanea sa
758	2	5.1	35	1	COPA_CANFA	P40765 canis famil

759	2	5.1	35	1	CPI2_PIG	P80736 sus scrofa
760	2	5.1	35	1	DEFB_MYTED	P81611 mytilus edu
761	2	5.1	35	1	END4_YEREN	P42691 yersinia en
762	2	5.1	35	1	FAS_CAPHI	P08757 capra hircu
763	2	5.1	35	1	FLAV_NOSSM	P35707 nostoc sp.
764	2	5.1	35	1	GBGU_MOUSE	Q61017 mus musculu
765	2	5.1	35	1	GP58_BPSP1	O48412 bacteriopha
766	2	5.1	35	1	GRDB_CLOPU	P55793 clostridium
767	2	5.1	35	1	GUR_GYMSY	P25810 gymnema syl
768	2	5.1	35	1	HCYA_CHEDE	P83173 cherax dest
769	2	5.1	35	1	HMWC_DESGI	P38588 desulfovibr
770	2	5.1	35	1	IAAC_HORVU	P34951 hordeum vul
771	2	5.1	35	1	KPPR_PINPS	P81664 pinus pinas
772	2	5.1	35	1	LCGB_LACLA	P36962 lactococcus
773	2	5.1	35	1	LEC1_CYTSE	P22970 cytisus ses
774	2	5.1	35	1	LEC3_ULEEU	P23032 ulex europe
775	2	5.1	35	1	PBP1_LYMDI	P34176 lymantria d
776	2	5.1	35	1	PBP_HYACE	P34175 hyalophora
777	2	5.1	35	1	PBP_ORGPS	P34178 orgyia pseu
778	2	5.1	35	1	PHI1_MYTCA	P35422 mytilus cal
779	2	5.1	35	1	PSAI_CYAPA	P48116 cyanophora
780	2	5.1	35	1	PSBM_SYN3	P72701 synechocyst
781	2	5.1	35	1	SCKG_PANIM	Q10726 pandinus im
782	2	5.1	35	1	SCKK_TITSE	P56219 tityus serr
783	2	5.1	35	1	SCX1_BUTSI	P15229 buthus sind
784	2	5.1	35	1	SPRC_PIG	P20112 sus scrofa
785	2	5.1	35	1	THPA_THADA	P21381 thaumatomococ
786	2	5.1	35	1	TMTX_MESTA	Q9bn12 mesobuthus
787	2	5.1	35	1	TX1_GRASP	P56852 grammastola
788	2	5.1	35	1	TX2_GRASP	P56853 grammastola
789	2	5.1	35	1	TXAG_AGEOP	P31328 agelena opu
790	2	5.1	35	1	TXH4_SELHU	P83303 selenocosmi
791	2	5.1	35	1	TXKS_STOHE	P29187 stoichactis
792	2	5.1	35	1	TXN4_SELHA	P83471 selenocosmi
793	2	5.1	35	1	VL3_PAPVD	P06919 deer papill
794	2	5.1	35	1	VSPA_CERVI	P18692 cerastes vi
795	2	5.1	35	1	Y210_HAEIN	P43964 haemophilus
796	2	5.1	35	1	Y320_BORBU	051299 borrelia bu
797	2	5.1	35	1	Y644_ARCFU	029613 archaeoglob
798	2	5.1	35	1	Y845_BORBU	051785 borrelia bu
799	2	5.1	35	1	Y847_BORBU	051787 borrelia bu
800	2	5.1	35	1	YC69_ARCFU	028999 archaeoglob
801	2	5.1	36	1	ANFV_ANGJA	P22642 anguilla ja
802	2	5.1	36	1	C3L1_BOVIN	P30922 bos taurus
803	2	5.1	36	1	CBBA_NITVU	P37102 nitrobacter
804	2	5.1	36	1	CYC7_GEOME	P81894 geobacter m
805	2	5.1	36	1	DESR_DESGI	P00273 desulfovibr
806	2	5.1	36	1	F4RE_METOG	P80951 methanogeni
807	2	5.1	36	1	GLU1_ORENI	P81026 oreochromis
808	2	5.1	36	1	GLUC_HYDCO	P09682 hydrolagus
809	2	5.1	36	1	H1L5_ENSMI	P27203 ensis minor
810	2	5.1	36	1	IAA_STRAU	P04082 streptomyce
811	2	5.1	36	1	IOB1_ISYOB	P58609 isyndus obs
812	2	5.1	36	1	KAD_STRGR	P53398 streptomyce
813	2	5.1	36	1	LHG_RHOVI	P04126 rhodopseudo
814	2	5.1	36	1	MFA1 YEAST	P34165 saccharomyc
815	2	5.1	36	1	NLTP_PINPI	P26912 pinus pinea

816	2	5.1	36	1	OST2_CHICK	P80897 gallus gall
817	2	5.1	36	1	PAHO_ALLMI	P06305 alligator m
818	2	5.1	36	1	PAHO_CERSI	P37999 ceratotheri
819	2	5.1	36	1	PAHO_CHIBR	P41519 chinchilla
820	2	5.1	36	1	PAHO_EQUZE	P38000 equus zebra
821	2	5.1	36	1	PAHO_ERIEU	P41335 erinaceus e
822	2	5.1	36	1	PAHO_MACMU	P33684 macaca mula
823	2	5.1	36	1	PAHO_RANCA	P15427 rana catesb
824	2	5.1	36	1	PAHO_RANTE	P31229 rana tempor
825	2	5.1	36	1	PAHO_TAPPI	P39659 tapirus pin
826	2	5.1	36	1	PETM_SYN3	P74810 synechocyst
827	2	5.1	36	1	PGKH_CHLFU	P36232 chlorella f
828	2	5.1	36	1	PMY_PETMA	P80024 petromyzon
829	2	5.1	36	1	PSAI_ANGLY	P28251 angiopteris
830	2	5.1	36	1	PSAI_BRAOL	Q31909 brassica ol
831	2	5.1	36	1	PSAI_CARCL	Q9gdv2 carpobrotus
832	2	5.1	36	1	PSAI_CHAGL	Q8m9x5 chaetosphae
833	2	5.1	36	1	PSAI_CHLVU	P58214 chlorella v
834	2	5.1	36	1	PSAI_CYACA	Q9tm24 cyanidium c
835	2	5.1	36	1	PSAI_GUITH	O78462 guillardia
836	2	5.1	36	1	PSAI_HORVU	P13165 hordeum vul
837	2	5.1	36	1	PSAI_MAIZE	P30980 zea mays (m
838	2	5.1	36	1	PSAI_MARPO	P12185 marchantia
839	2	5.1	36	1	PSAI_MESVI	Q9muq4 mesostigma
840	2	5.1	36	1	PSAI_NEPOL	Q9tl12 nephroselmi
841	2	5.1	36	1	PSAI_ORYSA	P12186 oryza sativ
842	2	5.1	36	1	PSAI_PICAB	O47040 picea abies
843	2	5.1	36	1	PSAI_PORPU	P51387 porphyra pu
844	2	5.1	36	1	PSAI_PSINU	Q8wi10 psilotum nu
845	2	5.1	36	1	PSAI_TOBAC	P12187 nicotiana t
846	2	5.1	36	1	PSAI_WHEAT	P25410 triticum ae
847	2	5.1	36	1	PSBI_ARATH	P09970 arabidopsis
848	2	5.1	36	1	PSBI_HORVU	P25876 hordeum vul
849	2	5.1	36	1	PSBI_MARPO	P09969 marchantia
850	2	5.1	36	1	PSBI_ORYSA	P12161 oryza sativ
851	2	5.1	36	1	PSBI_PINTH	P41599 pinus thunb
852	2	5.1	36	1	PSBI_PSEMZ	P29796 pseudotsuga
853	2	5.1	36	1	PSBM_CHLVU	P56325 chlorella v
854	2	5.1	36	1	PSBM_SYNEL	Q8dha7 synechococc
855	2	5.1	36	1	PYY_MYOSC	P09641 myoxocephal
856	2	5.1	36	1	PYY_ORENI	P81028 oreochromis
857	2	5.1	36	1	PYY_PIG	P01305 sus scrofa
858	2	5.1	36	1	PYY_RANRI	P29204 rana ridibu
859	2	5.1	36	1	RET4_CHICK	P30370 gallus gall
860	2	5.1	36	1	RL6_HALCU	P05968 halobacteri
861	2	5.1	36	1	SCK2_CENLL	P45630 centruroide
862	2	5.1	36	1	SCX1_BUTEU	P15220 buthus eupe
863	2	5.1	36	1	SCX8_BUTOC	P04098 buthus occi
864	2	5.1	36	1	SCXL_LEIQU	P45639 leiurus qui
865	2	5.1	36	1	SPYY_PHYBI	P80952 phylomedus
866	2	5.1	36	1	TERN_PSEUS	P82321 pseudacanth
867	2	5.1	36	1	TLN1_CHICK	P54939 gallus gall
868	2	5.1	36	1	TX1B_AGEAP	P15970 agelenopsis
869	2	5.1	36	1	TX35_PHONI	P81791 phoneutria
870	2	5.1	36	1	TXAM_METSE	P11495 metridium s
871	2	5.1	36	1	TXD3_PARLU	P83258 paracoelote
872	2	5.1	36	1	TXJA_HADVE	P82227 hadronyche

873	2	5.1	36	1	TXJB_HADVE	P82226 hadronyche
874	2	5.1	36	1	Y16L_BPT4	P39244 bacteriopha
875	2	5.1	36	1	Y260_BACHD	Q9kg53 bacillus ha
876	2	5.1	36	1	Y4KD_BPCHP	P19188 bacteriopha
877	2	5.1	36	1	Y609_ARCFU	O29646 archaeoglob
878	2	5.1	36	1	Y609_BORBU	O51554 borrelia bu
879	2	5.1	36	1	Y619_ARCFU	O29636 archaeoglob
880	2	5.1	36	1	YG50_HAEIN	P44281 haemophilus
881	2	5.1	36	1	YRKG_BACSU	P54434 bacillus su
882	2	5.1	37	1	AFP4_MALPA	P83138 malva parvi
883	2	5.1	37	1	ATPO_SOLTU	P80504 solanum tub
884	2	5.1	37	1	B2MG_ORENI	Q03423 oreochromis
885	2	5.1	37	1	CAL1_PIG	P30880 sus scrofa
886	2	5.1	37	1	CAL1_SHEEP	P30881 ovis aries
887	2	5.1	37	1	CG2S_LUPAN	P09930 lupinus ang
888	2	5.1	37	1	CS40_STAAU	P81684 staphylococ
889	2	5.1	37	1	CUP4_SARBU	P14486 sarcophaga
890	2	5.1	37	1	DEF4_ANDAU	P56686 androctonus
891	2	5.1	37	1	DEFA_MYTED	P81610 mytilus edu
892	2	5.1	37	1	ECAA_ECTTU	P49343 ectatomma t
893	2	5.1	37	1	ES2A_RANES	P40845 rana escula
894	2	5.1	37	1	ES2B_RANES	P40846 rana escula
895	2	5.1	37	1	F13A_BOVIN	P12260 bos taurus
896	2	5.1	37	1	IAPP_CRIGR	P19890 cricetus
897	2	5.1	37	1	LCNM_LACLA	P83002 lactococcus
898	2	5.1	37	1	LPPY_SERMA	P19937 serratia ma
899	2	5.1	37	1	MAUR_PARVE	Q56462 paracoccus
900	2	5.1	37	1	ME22_EUPRA	P58548 euplotes ra
901	2	5.1	37	1	MIBP_PSESP	P04576 pseudomonas
902	2	5.1	37	1	NLT3_VITSX	P80273 vitis sp. (
903	2	5.1	37	1	NLT4_VITSX	P80274 vitis sp. (
904	2	5.1	37	1	NUFM_SOLTU	P80266 solanum tub
905	2	5.1	37	1	OP2A_OXYKI	P83248 oxyopes kit
906	2	5.1	37	1	OP2B_OXYKI	P83249 oxyopes kit
907	2	5.1	37	1	OP2C_OXYKI	P83250 oxyopes kit
908	2	5.1	37	1	OP2D_OXYKI	P83251 oxyopes kit
909	2	5.1	37	1	PETG_ANASP	P58246 anabaena sp
910	2	5.1	37	1	PETG_ANAVA	Q913p7 anabaena va
911	2	5.1	37	1	PETG_ARATH	P56775 arabidopsis
912	2	5.1	37	1	PETG_CHAGL	Q8m9y4 chaetosphae
913	2	5.1	37	1	PETG_CHLEU	P46304 chlamydomon
914	2	5.1	37	1	PETG_CHLRE	Q08362 chlamydomon
915	2	5.1	37	1	PETG_CHLVU	P56305 chlorella v
916	2	5.1	37	1	PETG_CUSRE	P30398 cuscuta ref
917	2	5.1	37	1	PETG_CYAPA	P14236 cyanophora
918	2	5.1	37	1	PETG_EUGGR	P30396 euglena gra
919	2	5.1	37	1	PETG_GUITH	Q78505 guillardia
920	2	5.1	37	1	PETG_MARPO	P12120 marchantia
921	2	5.1	37	1	PETG_MESVI	Q9mun3 mesostigma
922	2	5.1	37	1	PETG_NEPOL	Q9tky8 nephroselmi
923	2	5.1	37	1	PETG_ODOSI	P49470 odontella s
924	2	5.1	37	1	PETG_ORYSA	P12121 oryza sativ
925	2	5.1	37	1	PETG_PINTH	P41614 pinus thunb
926	2	5.1	37	1	PETG_PSINU	Q8wi02 psilotum nu
927	2	5.1	37	1	PETG_SYNEL	Q8dki2 synechococc
928	2	5.1	37	1	PETG_SYNTP7	Q9z3g1 synechococc
929	2	5.1	37	1	PIIL_ACHLY	P81720 achromobact

930	2	5.1	37	1	POLN_WEEV	P13896 western equ
931	2	5.1	37	1	PRF1_RAT	P18889 rattus norv
932	2	5.1	37	1	PRT3_SCYCA	P30258 scyliorhinu
933	2	5.1	37	1	PSAI_ARATH	P56768 arabidopsis
934	2	5.1	37	1	PSAJ_EUGGR	P30394 euglena gra
935	2	5.1	37	1	PSBL_ARATH	P29301 arabidopsis
936	2	5.1	37	1	PSBL_ORYSA	P12166 oryza sativ
937	2	5.1	37	1	PSBM_PINTH	P41608 pinus thunb
938	2	5.1	37	1	PSBY_CYACA	O19893 cyanidium c
939	2	5.1	37	1	RK36_ARATH	P12144 arabidopsis
940	2	5.1	37	1	RK36_CHAGL	Q8m9v5 chaetosphae
941	2	5.1	37	1	RK36_CHLVU	P56360 chlorella v
942	2	5.1	37	1	RK36_CYACA	Q9tlu9 cyanidium c
943	2	5.1	37	1	RK36_CYAPA	P48131 cyanophora
944	2	5.1	37	1	RK36_EPIVI	P30069 epifagus vi
945	2	5.1	37	1	RK36_LOTJA	Q9bbq2 lotus japon
946	2	5.1	37	1	RK36_MARPO	P12142 marchantia
947	2	5.1	37	1	RK36_ODOSI	P49568 odontella s
948	2	5.1	37	1	RK36_OENHO	Q9mtj1 oenothera h
949	2	5.1	37	1	RK36_ORYSA	P12143 oryza sativ
950	2	5.1	37	1	RK36_PINTH	P41631 pinus thunb
951	2	5.1	37	1	RK36_PSINU	Q8why9 psilotum nu
952	2	5.1	37	1	RK36_SPIOL	P12230 spinacia ol
953	2	5.1	37	1	RL36_ANASP	Q8ypk0 anabaena sp
954	2	5.1	37	1	RL36_AQUAE	O66487 aquifex aeo
955	2	5.1	37	1	RL36_BACHD	O50631 bacillus ha
956	2	5.1	37	1	RL36_BACST	P07841 bacillus st
957	2	5.1	37	1	RL36_BACSU	P20278 bacillus su
958	2	5.1	37	1	RL36_BORBU	O51452 borrelia bu
959	2	5.1	37	1	RL36_CAMJE	Q9pm84 campylobact
960	2	5.1	37	1	RL36_CLOAB	Q97ek2 clostridium
961	2	5.1	37	1	RL36_CLOPE	Q8xhu7 clostridium
962	2	5.1	37	1	RL36_HAEIN	P46361 haemophilus
963	2	5.1	37	1	RL36_HELPJ	Q9zjt1 helicobacte
964	2	5.1	37	1	RL36_HELPY	P56058 helicobacte
965	2	5.1	37	1	RL36_LEPIN	Q9xd13 leptospira
966	2	5.1	37	1	RL36_LISMO	Q927n0 listeria mo
967	2	5.1	37	1	RL36_MYCGA	Q9rdv9 mycoplasma
968	2	5.1	37	1	RL36_MYCGE	P47420 mycoplasma
969	2	5.1	37	1	RL36_MYCPN	P52864 mycoplasma
970	2	5.1	37	1	RL36_MYCPU	Q98q05 mycoplasma
971	2	5.1	37	1	RL36_MYCSP	P38015 mycoplasma
972	2	5.1	37	1	RL36_NEIMA	Q9jrb2 neisseria m
973	2	5.1	37	1	RL36_PASMU	P57942 pasteurella
974	2	5.1	37	1	RL36_STAAM	Q99s42 staphylococ
975	2	5.1	37	1	RL36_SYNP6	O24707 synechococc
976	2	5.1	37	1	RL36_THETN	Q8r7x8 thermoanaer
977	2	5.1	37	1	RL36_TREPA	O83239 treponema p
978	2	5.1	37	1	RL36_UREPA	Q9pqn7 ureaplasma
979	2	5.1	37	1	RL36_VIBCH	P78001 vibrio chol
980	2	5.1	37	1	RL7_CLOPA	P05393 clostridium
981	2	5.1	37	1	RS15_HELLU	P52820 helix lucor
982	2	5.1	37	1	RUGC_RANRU	P80956 rana rugosa
983	2	5.1	37	1	SCK2_LEIQH	P45628 leiurus qui
984	2	5.1	37	1	SCK3_BUTOC	P59290 buthus occi
985	2	5.1	37	1	SCK3_PARTR	P83112 parabuthus
986	2	5.1	37	1	SCKA_TITSE	P46114 tityus serr

987	2	5.1	37	1	SCKC_LEIQH	P13487	leiurus qui
988	2	5.1	37	1	TX3D_AGEAP	P81746	agelenopsis
989	2	5.1	37	1	TXD1_PARLU	P83256	paracoelote
990	2	5.1	37	1	TXD2_PARLU	P83257	paracoelote
991	2	5.1	37	1	TXD4_PARLU	P83259	paracoelote
992	2	5.1	37	1	TXJC_HADVE	P82228	hadronyche
993	2	5.1	37	1	TXKB_BUNGR	P29186	bunodosoma
994	2	5.1	37	1	TXM2_AGEAP	P11058	agelenopsis
995	2	5.1	37	1	TXM4_AGEAP	P11060	agelenopsis
996	2	5.1	37	1	TXM5_AGEAP	P11061	agelenopsis
997	2	5.1	37	1	TXM6_AGEAP	P11062	agelenopsis
998	2	5.1	37	1	TXOF_HADVE	P81599	hadronyche
999	2	5.1	37	1	TXP3_APTSC	P49268	aptostichus
1000	2	5.1	37	1	VA1_BPBF2	P19347	bacteriopha

ALIGNMENTS

RESULT 1

PETL_ARATH

ID PETL_ARATH STANDARD; PRT; 31 AA.

AC P56776;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit petL).

GN PETL OR ATCG00590.

OS Arabidopsis thaliana (Mouse-ear cress).

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RX MEDLINE=20039611; PubMed=10574454;

RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;

RT "Complete structure of the chloroplast genome of Arabidopsis thaliana.";

RL DNA Res. 6:283-290(1999).

CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX.

CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated.

CC -!- SIMILARITY: Belongs to the petL family.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP000423; BAA84403.1; -.
DR HAMAP; MF_00433; -; 1.
DR Pfam; PF05115; PetL; 1.
KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;
KW Thylakoid.
FT TRANSMEM 4 24 POTENTIAL.
SQ SEQUENCE 31 AA; 3401 MW; BEE4295D2F2B854F CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLAAL 20
| | | | |
Db 11 LLAAL 15

RESULT 2
PETL_BETVU
ID PETL_BETVU STANDARD PRT; 31 AA.
AC P46612;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
DE petL).
GN PETL.
OS Beta vulgaris (Sugar beet).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
OX NCBI_TaxID=161934;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Altissima; TISSUE=Leaf;
RA Ran Z., Michaelis G.;
RT "Mapping of a chloroplast RFLP marker associated with the CMS
RT cytoplasm of sugar beet (Beta vulgaris).";
RL Theor. Appl. Genet. 91:836-840(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. TK81-O; TISSUE=Leaf;
RX MEDLINE=95254673; PubMed=7736615;
RA Kubo T., Yanai Y., Kinoshita T., Mikami T.;
RT "The chloroplast trnP-trnW-petG gene cluster in the mitochondrial
RT genomes of Beta vulgaris, B. trigyna and B. webbiana: evolutionary
RT aspects.";
RL Curr. Genet. 27:285-289(1995).
CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR
CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND
CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL
CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON
CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX.
CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated.

CC -!-- SIMILARITY: Belongs to the petL family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X87637; CAA60970.1; -.
DR EMBL; D38019; BAA07217.1; -.
DR EMBL; X87636; CAA60965.1; -.
DR PIR; T14568; T14568.
DR HAMAP; MF_00433; -; 1.
DR Pfam; PF05115; PetL; 1.
KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;
KW Thylakoid.
FT TRANSMEM 4 24 POTENTIAL.
SQ SEQUENCE 31 AA; 3400 MW; BEE4294AF46F754F CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
|||||
Db 11 LLAAL 15

RESULT 3
PETL_MAIZE
ID PETL_MAIZE STANDARD; PRT; 31 AA.
AC P19445;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
DE petL).
GN PETL.
OS Zea mays (Maize).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Haley J., Bogorad L.;
RL Submitted (MAY-1989) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95395841; PubMed=7666415;
RA Maier R.M., Neckermann K., Igloi G.L., Koessel H.;
RT "Complete sequence of the maize chloroplast genome: gene content,
RT hotspots of divergence and fine tuning of genetic information by
RT transcript editing.";

RL J. Mol. Biol. 251:614-628 (1995).
CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR
CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND
CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL
CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON
CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX.
CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated.
CC -!- SIMILARITY: Belongs to the petL family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J04502; AAA84479.1; -.
DR EMBL; X86563; CAA60303.1; -.
DR PIR; S58569; S58569.
DR MaizeDB; 69195; -.
DR HAMAP; MF_00433; -; 1.
DR Pfam; PF05115; PetL; 1.
KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;
KW Thylakoid.
FT TRANSMEM 4 24 POTENTIAL.
SQ SEQUENCE 31 AA; 3456 MW; 0AE4294FA7E8B48E CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
|||
Db 11 LLAAL 15

RESULT 4
PETL_OENHO
ID PETL_OENHO STANDARD PRT; 31 AA.
AC Q9MTK4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
DE petL).
GN PETL.
OS Oenothera hookeri (Hooker's evening primrose).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;
OC eurosids II; Myrtales; Onagraceae; Oenothera.
OX NCBI_TaxID=85636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Johansen;
RX MEDLINE=20309318; PubMed=10852478;

RA Hupfer H., Swiatek M., Hornung S., Herrmann R.G., Maier R.M.,
RA Chiu W.-L., Sears B.;
RT "Complete nucleotide sequence of the Oenothera elata plastid
RT chromosome, representing plastome I of the five distinguishable
RT Euoenothera plastomes.";
RL Mol. Genet. 263:581-585 (2000).
CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR
CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND
CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL
CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON
CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
CC similarity).
CC -!- SIMILARITY: Belongs to the petL family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ271079; CAB67175.1; -.
DR HAMAP; MF_00433; -; 1.
DR Pfam; PF05115; PetL; 1.
KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;
KW Thylakoid.
FT TRANSMEM 4 24 POTENTIAL.
SQ SEQUENCE 31 AA; 3415 MW; A015C65D2F325493 CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
|||
Db 11 LLAAL 15

RESULT 5
PETL_ORYSA
ID PETL_ORYSA STANDARD; PRT; 31 AA.
AC P12180;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
DE petL).
GN PETL.
OS Oryza sativa (Rice).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RX MEDLINE=89364698; PubMed=2770692;
 RA Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
 RA Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
 RA Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugiura M.;
 RT "The complete sequence of the rice (*Oryza sativa*) chloroplast genome:
 RT intermolecular recombination between distinct tRNA genes accounts for
 RT a major plastid DNA inversion during the evolution of the cereals.";
 RL Mol. Genet. 217:185-194(1989).
 CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR
 CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND
 CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL
 CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON
 CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX.
 CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated.
 CC -!- SIMILARITY: Belongs to the petL family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X15901; CAA33966.1; -.
 DR PIR; S05124; S05124.
 DR Gramene; P12180; -.
 DR HAMAP; MF_00433; -; 1.
 DR Pfam; PF05115; PetL; 1.
 KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;
 KW Thylakoid.
 FT TRANSMEM 4 24 POTENTIAL.
 SQ SEQUENCE 31 AA; 3442 MW; BEE4294FBC84B0C2 CRC64;

 Query Match 12.8%; Score 5; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 16 LLAAL 20
 |||||
 Db 11 LLAAL 15

 RESULT 6
 PETL_PSIINU
 ID PETL_PSIINU STANDARD; PRT; 31 AA.
 AC Q8WI03;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
 DE petL).
 GN PETL.
 OS Psilotum nudum (Whisk fern).

OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Psilotophyta; Psilotales; Psilotaceae; Psilotum.
OX NCBI_TaxID=3240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Kingyoku;
RA Wakasugi T., Nishikawa A., Yamada K., Sugiura M.;
RT "Complete nucleotide sequence of the chloroplast genome from a fern,
RT Psilotum nudum.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: The cytochrome b6-f complex functions in the linear
CC cross-membrane transport of electrons between photosystem II and
CC I, as well as in cyclic electron flow around photosystem I. PetL
CC is important for photoautotrophic growth as well as for electron
CC transfer efficiency and stability of the cytochrome b6-f complex.
CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
CC similarity).
CC -!- SIMILARITY: Belongs to the petL family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP004638; BAB84234.1; -.
DR HAMAP; MF_00433; -; 1.
DR Pfam; PF05115; PetL; 1.
KW Electron transport; Respiratory chain; Transmembrane; Thylakoid;
KW Chloroplast.
SQ SEQUENCE 31 AA; 3392 MW; 84D427FB6FDCC51B CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
|||
Db 11 LLAAL 15

RESULT 7
PETL_SPIOL
ID PETL_SPIOL STANDARD; PRT; 31 AA.
AC Q9M3L0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
DE petL).
GN PETL.
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Geant d'hiver, and cv. Monatol;
RX MEDLINE=21187424; PubMed=11292076;
RA Schmitz-Linneweber C., Maier R.M., Alcaraz J.-P., Cottet A.,
RA Herrmann R.G., Mache R.;
RT "The plastid chromosome of spinach (*Spinacia oleracea*): complete
RT nucleotide sequence and gene organization.";
RL Plant Mol. Biol. 45:307-315(2001).
CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR
CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND
CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL
CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON
CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
CC similarity).
CC -!- SIMILARITY: Belongs to the petL family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ400848; CAB88746.1; -.
DR HAMAP; MF_00433; -; 1.
DR Pfam; PF05115; PetL; 1.
KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;
KW Thylakoid.
FT TRANSMEM 4 24 POTENTIAL.
SQ SEQUENCE 31 AA; 3390 MW; BEE4294AF46C457C CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
|||
Db 11 LLAAL 15

RESULT 8
PETL_TOBAC
ID PETL_TOBAC STANDARD PRT; 31 AA.
AC P12181;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
DE petL).
GN PETL.

OS Nicotiana tabacum (Common tobacco).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bright Yellow 4;
RA Shinozaki K., Ohme M., Tanaka M., Wakasugi T., Hayashida N.,
RA Matsubayashi T., Zaita N., Chunwongse J., Obokata J.,
RA Yamaguchi-Shinozaki K., Ohto C., Torazawa K., Meng B.-Y., Sugita M.,
RA Deno H., Kamogashira T., Yamada K., Kusuda J., Takaiwa F., Kato A.,
RA Tohdoh N., Shimada H., Sugiura M.;
RT "The complete nucleotide sequence of the tobacco chloroplast genome:
its gene organization and expression.";
RL EMBO J. 5:2043-2049(1986).
CC -!-- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR
CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND
CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL
CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON
CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX.
CC -!-- SUBCELLULAR LOCATION: Thylakoid membrane-associated.
CC -!-- SIMILARITY: Belongs to the petL family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z00044; CAA77419.1; -.
DR HAMAP; MF_00433; -; 1.
DR Pfam; PF05115; PetL; 1.
KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;
KW Thylakoid.
FT TRANSMEM 4 24 POTENTIAL.
SQ SEQUENCE 31 AA; 3389 MW; BEE4294FA4364493 CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
|||
Db 11 LLAAL 15

RESULT 9
PETL_WHEAT
ID PETL_WHEAT STANDARD PRT; 31 AA.
AC P58247;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
DE petL).
GN PETL.
OS Triticum aestivum (Wheat).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Chinese Spring;
RA Ogihara Y., Isono K., Kojima T., Endo A., Hanaoka M., Shiina T.,
RA Terachi T., Utsugi S., Murata M., Mori N., Takumi S., Ikeo K.,
RA Gojobori T., Murai R., Murai K., Matsuoka Y., Ohnishi Y., Tajiri H.,
RA Tsunewaki K.;
RT "Chinese spring wheat (*Triticum aestivum* L.) chloroplast genome:
complete sequence and contig clones.";
RL Plant Mol. Biol. Rep. 18:243-253(2000).
CC --!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR
CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND
CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL
CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON
CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
CC similarity).
CC -!- SIMILARITY: Belongs to the petL family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB042240; BAB47051.1; -.
DR HAMAP; MF_00433; -; 1.
DR Pfam; PF05115; PetL; 1.
KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;
KW Thylakoid.
FT TRANSMEM 4 24 POTENTIAL.
SQ SEQUENCE 31 AA; 3426 MW; BEE4294AF7BDB493 CRC64;

Query Match 12.8%; Score 5; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAAL 20
| | | | |
Db 11 LLAAL 15

RESULT 10
REV_SIVM2
ID REV_SIVM2 STANDARD; PRT; 37 AA.

AC P08809;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE REV protein (Anti-repression transactivator protein) (ART/TRS)
DE (Fragment).
GN REV.
OS Simian immunodeficiency virus (Mm251 isolate) (SIV-MAC).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11734;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88122665; PubMed=2893293;
RA Kestler H.W., Li Y., Naidu Y.M., Butler C.V., Ochs M.F., Jaenel G.,
RA King N.W., Daniel M.D., Desrosiers R.C.;
RT "Comparison of simian immunodeficiency virus isolates.";
RL Nature 331:619-622(1988).
CC -!- FUNCTION: REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE
CC NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.
CC -!- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.
CC -!- PTM: PHOSPHOPROTEIN WHOSE STATE OF PHOSPHORYLATION IS MEDIATED
CC BY A SPECIFIC SERINE KINASE ACTIVITY PRESENT IN THE NUCLEUS.
CC -!- MISCELLANEOUS: THIS IS A MACAQUE ISOLATE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X06879; -; NOT_ANNOTATED_CDS.
DR HIV; X06879; REV\$MM251.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
KW Transcription regulation; AIDS; Phosphorylation; Nuclear protein.
FT NON_TER 1 1
FT NON_TER 37 37
SQ SEQUENCE 37 AA; 4633 MW; 059C315CC56C5583 CRC64;

Query Match 12.8%; Score 5; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALAD 6
||| |
Db 28 LALAD 32

RESULT 11
PA22_MICNI
ID PA22_MICNI STANDARD; PRT; 28 AA.
AC P21791;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Phospholipase A2 isozyme 2 (EC 3.1.1.4) (Phosphatidylcholine
 DE 2-acylhydrolase) (Fragment).
 OS Micrurus nigrocinctus (Central American coral snake) (Gargantilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Micrurus.
 OX NCBI_TaxID=8635;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Mochca-Morales J., Martin B.M., Zamudio F.Z., Possani L.D.;
 RT "Isolation and characterization of three toxic phospholipases from
 RT the venom of the coral snake *Micrurus nigrocinctus*.";
 RL Toxicon 28:616-617(1990).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides. Inhibits neuromuscular
 CC transmission by blocking acetylcholine release from the nerve
 CC termini. Acts presynaptically.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP I
 CC SUBFAMILY.
 DR PIR; B35948; B35948.
 DR HSSP; P15445; 1A3D.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR Pfam; PF00068; phoslip; 1.
 DR ProDom; PD000303; PhospholipaseA2; 1.
 DR PROSITE; PS00119; PA2 ASP; PARTIAL.
 DR PROSITE; PS00118; PA2 HIS; PARTIAL.
 KW Hydrolase; Lipid degradation; Calcium; Toxin; Neurotoxin;
 KW Presynaptic neurotoxin; Multigene family.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3373 MW; 6979B52DF2D718BC CRC64;

Query Match 10.3%; Score 4; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 23 RHWL 26
 ||||
 Db 15 RHWL 18

RESULT 12
 PETL_CYAPA
 ID PETL_CYAPA STANDARD; PRT; 28 AA.
 AC P48102;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
 DE petL).
 GN PETL.
 OS Cyanophora paradoxa.
 OG Cyanelle.

OC Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.
OX NCBI_TaxID=2762;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UTEX LB 555 / Pringsheim;
RA Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
RA Bryant D.A.;
RT "Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa.";
RL Plant Mol. Biol. Rep. 13:327-332(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=UTEX LB 555 / Pringsheim;
RA Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M.,
RA Farley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C.,
RA Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
RT "The complete sequence of the cyanelle genome of Cyanophora paradoxa:
the genetic complexity of a primitive plastid.";
RL (In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
RL Schwemmler W. (eds.);
RL Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg
RL (1997).
CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR
CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND
CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL
CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON
CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX.
CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated.
CC -!- SIMILARITY: Belongs to the petL family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U30821; AAA81268.1; -.
DR PIR; T06925; T06925.
DR HAMAP; MF_00433; -; 1.
KW Electron transport; Cyanelle; Respiratory chain; Transmembrane;
KW Thylakoid.
FT TRANSMEM 2 22 POTENTIAL.
SQ SEQUENCE 28 AA; 3106 MW; ADAE8353D596AF3C CRC64;

Query Match 10.3%; Score 4; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LALA 5
|||
Db 14 LALA 17

RESULT 13
PETN_GUITH
ID PETN_GUITH STANDARD PRT; 29 AA.

AC O78498;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b6-f complex subunit VIII (Cytochrome b6f complex subunit
 DE petN).
 GN PETN OR YCF6.
 OS Guillardia theta (Cryptomonas phi).
 OG Chloroplast.
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
 OX NCBI_TaxID=55529;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99128221; PubMed=9929392;
 RA Douglas S.E., Penny S.L.;
 RT "The plastid genome of the cryptophyte alga, Guillardia theta:
 RT complete sequence and conserved synteny groups confirm its common
 RT ancestry with red algae.";
 RL J. Mol. Evol. 48:236-244(1999).
 CC -!- FUNCTION: PLAYS A CRUCIAL ROLE IN CYTOCHROME B6-F COMPLEX ASSEMBLY
 CC AND/OR STABILITY (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the petN family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF041468; AAC35689.1; -.
 DR HAMAP; MF_00395; -; 1.
 DR InterPro; IPR005497; PetN.
 DR Pfam; PF03742; PetN; 1.
 KW Electron transport; Chloroplast; Respiratory chain; Thylakoid;
 KW Transmembrane.
 FT TRANSMEM 3 23 POTENTIAL.
 SQ SEQUENCE 29 AA; 3231 MW; 13FB2B1B7B3525BD CRC64;

 Query Match 10.3%; Score 4; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SLAL 4
 ||||
 Db 18 SLAL 21

RESULT 14
 PETN_ODOSI
 ID PETN_ODOSI STANDARD PRT 29 AA.
 AC P49527;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b6-f complex subunit VIII (Cytochrome b6f complex subunit
DE petN).
GN PETN OR YCF6.
OS Odontella sinensis (Marine centric diatom).
OG Chloroplast.
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
OC Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella.
OX NCBI_TaxID=2839;
RN [1]
RP SEQUENCE FROM N.A.
RA Kowallik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freier U.;
RT "The chloroplast genome of a chlorophyll a+c-containing alga,
RT Odontella sinensis.";
RL Plant Mol. Biol. Rep. 13:336-342(1995).
CC -!- FUNCTION: PLAYS A CRUCIAL ROLE IN CYTOCHROME B6-F COMPLEX ASSEMBLY
CC AND/OR STABILITY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
CC similarity).
CC -!- SIMILARITY: Belongs to the petN family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z67753; CAA91699.1; - .
DR PIR; S78326; S78326.
DR HAMAP; MF_00395; - ; 1.
DR InterPro; IPR005497; PetN.
DR Pfam; PF03742; PetN; 1.
KW Electron transport; Chloroplast; Respiratory chain; Thylakoid;
KW Transmembrane.
FT TRANSMEM 3 23 POTENTIAL.
SQ SEQUENCE 29 AA; 3249 MW; E1589B4ABBB4C5A0 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLAL 4
Db 18 SLAL 21

RESULT 15
PETN_SKECO
ID PETN_SKECO STANDARD PRT; 29 AA.
AC O96807;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b6-f complex subunit VIII (Cytochrome b6f complex subunit
DE petN).

GN YCF6.
OS Skeletonema costatum (Marine centric diatom).
OG Chloroplast.
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
OC Thalassiosiophycidae; Thalassiosirales; Skeletonemataceae;
OC Skeletonema.
OX NCBI_TaxID=2843;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIES-323;
RA Tada N., Otsuka S., Oyaizu H., Matsumoto S.;
RT "Plastid DNA sequences of Skeletonema costatum NIES 323.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: PLAYS A CRUCIAL ROLE IN CYTOCHROME B6-F COMPLEX ASSEMBLY
CC AND/OR STABILITY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
CC similarity).
CC -!- SIMILARITY: Belongs to the petN family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ132265; CAA10628.1; -.
DR HAMAP; MF_00395; -; 1.
DR InterPro; IPR005497; PetN.
DR Pfam; PF03742; PetN; 1.
KW Electron transport; Chloroplast; Respiratory chain; Thylakoid;
KW Transmembrane.
FT TRANSMEM 3 23 POTENTIAL.
SQ SEQUENCE 29 AA; 3221 MW; E1588B90DE14C5A0 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLAL 4
|||
Db 18 SLAL 21

RESULT 16
PETN_CYACA
ID PETN_CYACA STANDARD PRT; 31 AA.
AC Q9TLR6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b6-f complex subunit VIII (Cytochrome b6f complex subunit
DE petN).
GN PETN OR YCF42.
OS Cyanidium caldarium.
OG Chloroplast.

OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
OC Cyanidium.
OX NCBI_TaxID=2771;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RK-1;
RX MEDLINE=20496959; PubMed=11040290;
RA Gloeckner G., Rosenthal A., Valentin K.-U.;
RT "The structure and gene repertoire of an ancient red algal plastid
RT genome.";
RL J. Mol. Evol. 51:382-390(2000).
CC -!- FUNCTION: PLAYS A CRUCIAL ROLE IN CYTOCHROME B6-F COMPLEX ASSEMBLY
CC AND/OR STABILITY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
CC similarity).
CC -!- SIMILARITY: Belongs to the petN family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF022186; AAF12891.1; -.
DR HAMAP; MF_00395; -; 1.
DR InterPro; IPR005497; PetN.
DR Pfam; PF03742; PetN; 1.
KW Electron transport; Chloroplast; Respiratory chain; Thylakoid;
KW Transmembrane.
FT TRANSMEM 5 25 POTENTIAL.
SQ SEQUENCE 31 AA; 3458 MW; 79D1E8E4E2493319 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLAL 4
| || |
Db 20 SLAL 23

RESULT 17
PSAM_CHLVU
ID PSAM_CHLVU STANDARD; PRT; 31 AA.
AC P56314;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Photosystem I reaction centre subunit XII (PSI-M).
GN PSAM.
OS Chlorella vulgaris.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
OX NCBI_TaxID=3077;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IAM C-27 / Tamiya;
 RX MEDLINE=97303241; PubMed=9159184;
 RA Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,
 RA Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T.,
 RA Inamura A., Yoshinaga K., Sugiura M.;
 RT "Complete nucleotide sequence of the chloroplast genome from the
 green alga Chlorella vulgaris: the existence of genes possibly
 involved in chloroplast division.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).
 CC -!- SIMILARITY: BELONGS TO THE PSAM FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB001684; BAA57938.1; -.
 DR PIR; T07290; T07290.
 KW Photosystem I; Photosynthesis; Chloroplast.
 SQ SEQUENCE 31 AA; 3310 MW; 184858F3D8BD6873 CRC64;

 Query Match 10.3%; Score 4; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 2 LALA 5
 ||||
 Db 14 LALA 17

RESULT 18
 PSAM_SYNY3
 ID PSAM_SYNY3 STANDARD PRT; 31 AA.
 AC P72986;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Photosystem I reaction centre subunit XII (PSI-M).
 GN PSAM OR SMR0005.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
 RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
 RA Yamada M., Yasuda M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the

RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- SIMILARITY: BELONGS TO THE PSAM FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D90902; BAA17005.1; -.
DR PIR; S74965; S74965.
KW Photosystem I; Photosynthesis; Complete proteome.
SQ SEQUENCE 31 AA; 3380 MW; 07E0E7E8CB2720F0 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LAAL 20
||||
Db 9 LAAL 12

RESULT 19
PSBZ_EUGST
ID PSBZ_EUGST STANDARD; PRT; 32 AA.
AC Q8SL89;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Photosystem II reaction center Z protein (Fragment).
GN PSBZ OR YCF9.
OS Euglena stellata.
OG Chloroplast.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
OX NCBI_TaxID=38278;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21851312; PubMed=11861918;
RA Sheveleva E.V., Giordani N.V., Hallick R.B.;
RT "Identification and comparative analysis of the chloroplast alpha-
RT subunit gene of DNA-dependent RNA polymerase from seven Euglena
RT species.";
RL Nucleic Acids Res. 30:1247-1254(2002).
CC -!- FUNCTION: Controls the interaction of photosystem II (PSII) cores
CC with the light-harvesting antenna (By similarity).
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
CC with the photosystem II complex (By similarity).
CC -!- SIMILARITY: Belongs to the psbZ family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY047486; AAL83365.1; -.
DR HAMAP; MF_00644; -; 1.
KW Photosynthesis; Photosystem II; Reaction center; Thylakoid;
KW Transmembrane; Chloroplast.
FT NON_TER 1 1
FT TRANSMEM 11 31 POTENTIAL.
SQ SEQUENCE 32 AA; 3566 MW; 9414D7D307878309 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 LNSY 29
|||
Db 27 LNSY 30

RESULT 20

PBAN_LYMDI
ID PBAN_LYMDI STANDARD; PRT; 33 AA.
AC P43511;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Pheromone biosynthesis activating neuropeptide (LYD-PBAN).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Suboesophageal ganglion;
RX MEDLINE=95072631; PubMed=7981730;
RA Masler E.P., Raina A.K., Wagner R.M., Kochansky J.P.;
RT "Isolation and identification of a pheromonotropic neuropeptide from
RT the brain-suboesophageal ganglion complex of Lymantria dispar: a new
RT member of the PBAN family.";
RL Insect Biochem. Mol. Biol. 24:829-836(1994).
CC -!- FUNCTION: INVOLVED IN THE CONTROL OF PHEROMONE PRODUCTION IN
CC FEMALE GYPSY MOTH.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Hormone; Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 33 33 AMIDATION.
SQ SEQUENCE 33 AA; 3884 MW; E4CB1B8AFD3FEFC2 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LADD 7

Db

||||
1 LADD 4

RESULT 21

YC12_MARPO

ID YC12_MARPO STANDARD; PRT; 33 AA.

AC P31560;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical 3.4 kDa protein ycf12 (ORF 33).

GN YCF12.

OS Marchantia polymorpha (Liverwort).

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;

OC Marchantiopsida; Marchantiidae; Marchantiales; Marchantiineae;

OC Marchantiaceae; Marchantia.

OX NCBI_TaxID=3197;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89068687; PubMed=3199436;

RA Fukuzawa H., Kohchi T., Sano T., Shirai H., Umesono K., Inokuchi H.,

RA Ozeki H., Ohyama K.;

RT "Structure and organization of Marchantia polymorpha chloroplast

RT genome. III. Gene organization of the large single copy region from

RT rbcL to trnI(CAU).";

RL J. Mol. Biol. 203:333-351(1988).

RN [2]

RP SEQUENCE FROM N.A.

RA Ohyama K., Fukuzawa H., Kohchi T., Shirai H., Sano T., Sano S.,

RA Umesono K., Shiki Y., Takeuchi M., Chang Z., Aota S., Inokuchi H.,

RA Ozeki H.;

RT "Chloroplast gene organization deduced from complete sequence of

RT liverwort Marchantia polymorpha chloroplast DNA.";

RL Nature 322:572-574(1986).

CC -!- SIMILARITY: BELONGS TO THE YCF12 FAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; X04465; CAA28069.1; -.

DR PIR; S01581; A05010.

KW Chloroplast; Hypothetical protein.

SQ SEQUENCE 33 AA; 3386 MW; C88B5B778FF1C50D CRC64;

Query Match 10.3%; Score 4; DB 1; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

16 LLAA 19

||||

Db 25 LLAA 28

RESULT 22
PETG_CYACA
ID PETG_CYACA STANDARD; PRT; 35 AA.
AC Q9TLQ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b6-f complex subunit V (Cytochrome b6f complex subunit
DE petG).
GN PETG.
OS Cyanidium caldarium.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
OC Cyanidium.
OX NCBI_TaxID=2771;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RK-1;
RX MEDLINE=20496959; PubMed=11040290;
RA Gloeckner G., Rosenthal A., Valentin K.-U.;
RT "The structure and gene repertoire of an ancient red algal plastid
RT genome.";
RL J. Mol. Evol. 51:382-390(2000).
CC -!- FUNCTION: The cytochrome b6-f complex functions in the linear
CC cross-membrane transport of electrons between photosystem II and
CC I, as well as in cyclic electron flow around photosystem I. PetG
CC is required for either the stability or assembly of the cytochrome
CC b6-f complex (By similarity).
CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated.
CC -!- SIMILARITY: Belongs to the petG family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF022186; AAF12884.1; -.
DR HAMAP; MF_00432; -; 1.
DR InterPro; IPR003683; Cytochrmb6/f_5.
DR Pfam; PF02529; PetG; 1.
KW Electron transport; Chloroplast; Respiratory chain; Thylakoid;
KW Transmembrane.
FT DOMAIN 1 4 LUMENAL (POTENTIAL).
FT TRANSMEM 5 25 POTENTIAL.
FT DOMAIN 26 35 STROMAL (POTENTIAL).
SQ SEQUENCE 35 AA; 3803 MW; B03C27094A1B74F3 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAA 19
 ||||
Db 21 LLAA 24

RESULT 23

PYY_RAJRH

ID PYY_RAJRH STANDARD; PRT; 36 AA.
AC P29206;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Peptide YY-like (PYY).
OS Raja rhina (Skate).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
OC Rajiformes; Rajidae; Raja.
OX NCBI_TaxID=30478;
RN [1]
RP SEQUENCE.
RX MEDLINE=91296574; PubMed=2067973;
RA Conlon J.M., Bjenning C., Moon T.W., Youson J.H., Thim L.;
RT "Neuropeptide Y-related peptides from the pancreas of a teleostean
eel), holostean (bowfin) and elasmobranch (skate) fish.";
RL Peptides 12:221-226(1991).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the NPY family.
DR HSSP; P01303; 1RON.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3; 1.
DR PRINTS; PR00278; PANCHORMONE.
DR ProDom; PD001267; Pancreatic_hormn; 1.
DR SMART; SM00309; PAH; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
KW Hormone; Amidation.
FT MOD_RES 36 36 AMIDATION.
SQ SEQUENCE 36 AA; 4251 MW; 07A7D9DC196660B6 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DDAA 9
 ||||
Db 10 DDAA 13

RESULT 24

DIU1_TENMO

ID DIU1_TENMO STANDARD; PRT; 37 AA.
AC P56618;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Diuretic hormone I (DH I) (Diuretic peptide I) (DP I) (DH(37)).
OS Tenebrio molitor (Yellow mealworm).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=96109258; PubMed=8618894;
RA Furuya K., Schegg K.M., Wang H., King D.S., Schooley D.A.;
RT "Isolation and identification of a diuretic hormone from the mealworm
RT *Tenebrio molitor*.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:12323-12327(1995).
CC -!- FUNCTION: Increases cyclic AMP production in Malpighian tubules.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
CC FACTOR/UROTENSIN I FAMILY OF PEPTIDES.
DR PIR; A58607; A57127.
DR InterPro; IPR000187; corticoliberin.
DR Pfam; PF00473; CRF; 1.
DR SMART; SM00039; CRF; 1.
DR PROSITE; PS00511; CRF; 1.
KW Hormone.
SQ SEQUENCE 37 AA; 4371 MW; 519EC232D3473A85 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ERAR 15
|||
Db 20 ERAR 23

RESULT 25
RK36_NEPOL
ID RK36_NEPOL STANDARD PRT; 37 AA.
AC Q9TL26;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chloroplast 50S ribosomal protein L36.
GN RPL36.
OS Nephroelmis olivacea.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
OC Chlorodendrales; Chlorodendraceae; Nephroelmis.
OX NCBI_TaxID=31312;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIES-484;
RX MEDLINE=99398694; PubMed=10468594;
RA Turmel M., Otis C., Lemieux C.;
RT "The complete chloroplast DNA sequence of the green alga *Nephroelmis*
RT *olivacea*: insights into the architecture of ancestral chloroplast
RT genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).
CC -!- SIMILARITY: BELONGS TO THE L36P FAMILY OF RIBOSOMAL PROTEINS.

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AF137379; AAD54790.1; -.
DR HSSP; P80256; 1DFE.
DR HAMAP; MF_00251; -; 1.
DR InterPro; IPR000473; Ribosomal_L36.
DR Pfam; PF00444; Ribosomal_L36; 1.
DR ProDom; PD002101; Ribosomal_L36; 1.
DR TIGRFAMs; TIGR01022; rpmJ_bact; 1.
DR PROSITE; PS00828; RIBOSOMAL_L36; 1.
KW Ribosomal protein; Chloroplast.
SQ SEQUENCE 37 AA; 4429 MW; BC68BD516BF7FB37 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 KLLV 35
|||
Db 22 KLLV 25

RESULT 26
CPRP_CANPG
ID CPRP_CANPG STANDARD; PRT; 38 AA.
AC P81033;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE CHH precursor related peptide (CPRP).
OS Cancer pagurus (Rock crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Cancroidea; Cancridae; Cancer.
OX NCBI_TaxID=6755;
RN [1]
RP SEQUENCE.
RC TISSUE=Sinus gland;
RX MEDLINE=99025664; PubMed=9809792;
RA Chung J.S., Wilkinson M.C., Webster S.G.;
RT "Amino acid sequences of both isoforms of crustacean hyperglycemic
RT hormone (CHH) and corresponding precursor-related peptide in Cancer
RT pagurus.";
RL Regul. Pept. 77:17-24(1998).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PRODUCED BY THE MEDULLA TERMINALIS X-ORGAN IN
CC THE EYESTALKS AND TRANSPORTED TO THE SINUS GLAND WHERE IT IS
CC STORED AND RELEASED.
DR InterPro; IPR005558; Crust_neuro_H.
DR Pfam; PF03858; Crust_neuro_H; 1.

KW Neuropeptide; Hormone.
SQ SEQUENCE 38 AA; 3969 MW; C979C87EE31ABB90 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 RLLA 18
||||
Db 11 RLLA 14

RESULT 27
GVPC_SPICC
ID GVPC_SPICC STANDARD; PRT; 39 AA.
AC P81000;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gas vesicle protein C (Fragment).
GN GVPC.
OS Spirulina sp. (strain CCAP 1475/10).
OC Bacteria; Cyanobacteria; Oscillatoriales; Spirulina.
OX NCBI_TaxID=69016;
RN [1]
RP SEQUENCE.
RX MEDLINE=92407497; PubMed=1527496;
RA Griffiths A.E., Walsby A.E., Hayes P.K.;
RT "The homologies of gas vesicle proteins.";
RL J. Gen. Microbiol. 138:1243-1250(1992).
CC -!- FUNCTION: May confer stability to the gas vesicle membranes. Gas vesicles are small, hollow, gas filled protein structures that are found in several microbial planktonic microorganisms. They allow the positioning of the organism at the favorable depth for growth.
CC -!- SUBCELLULAR LOCATION: BINDS TO THE EXTERNAL SURFACE OF THE GAS VESICLE MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE GAS VESICLE PROTEIN TYPE C FAMILY.
DR InterPro; IPR002003; Gas_vesicle_C.
DR PROSITE; PS00235; GAS_VESICLE_C; PARTIAL.
KW Gas vesicle.

FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4487 MW; D9980C1C0CF459E7 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 LERR 23
||||
Db 11 LERR 14

RESULT 28
NPF_MONEX
ID NPF_MONEX STANDARD; PRT; 39 AA.
AC P41967;

DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neuropeptide F (NPY).
OS Moniezia expansa (Sheep tapeworm).
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidea; Anoplocephalidae; Moniezia.
OX NCBI_TaxID=28841;
RN [1]
RP SEQUENCE.
RA Maule A.G., Shaw C., Halton D.W., Thim L., Johnston C.F.,
RA Fairweather I., Buchanan K.D.;
RT "Neuropeptide F: a novel parasitic flatworm regulatory peptide from
RT Moniezia expansa (Cestoda: Cyclophyllidea).";
RL Parasitology 102:309-316(1991).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=93096525; PubMed=1461689;
RA Maule A.G., Shaw C., Halton D.W., Brennan G.P., Johnston C.F.,
RA Moore S.;
RT "Neuropeptide F (Moniezia expansa): localization and characterization
RT using specific antisera.";
RL Parasitology 105:505-512(1992).
CC -!- FUNCTION: MAY HAVE AN IMPORTANT PHYSIOLOGICAL ROLE IN
CC NEUROREGULATION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the NPY family.
DR PDB; 1K8V; 12-JUN-02.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3; 1.
DR SMART; SM00309; PAH; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
KW Neuropeptide; Amidation; 3D-structure.
FT MOD_RES 39 39 AMIDATION.
SQ SEQUENCE 39 AA; 4594 MW; 2D61A76927DEA732 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 LVLD 37
|||
Db 12 LVLD 15

RESULT 29
PHRI_BACSU
ID PHRI_BACSU STANDARD; PRT; 39 AA.
AC O31492;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatase rapI inhibitor (Phosphatase regulator I).
GN PHRI.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borrius R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenerger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -!- FUNCTION: Inhibitor of the activity of phosphatase rapI.
CC -!- SIMILARITY: BELONGS TO THE PHR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z99106; CAB12309.1; -.
DR PIR; E69677; E69677.
DR SubtiList; BG12645; phrI.
KW Complete proteome.
SQ SEQUENCE 39 AA; 4232 MW; 5C716F587894B2DA CRC64;

Query Match 10.3%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLAA 19
 |||||
Db 7 LLAA 10

RESULT 30
THIO_CLOSG
ID THIO_CLOSG STANDARD; PRT; 40 AA.
AC P81108;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thioredoxin (TRX) (Fragment).
GN TRXA.
OS Clostridium sporogenes.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1509;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 633;
RX MEDLINE=98195737; PubMed=9534247;
RA Harms C., Meyer M.A., Andreesen J.R.;
RT "Fast purification of thioredoxin reductases and of thioredoxins with
RT an unusual redox-active centre from anaerobic, amino-acid-utilizing
RT bacteria.";
RL Microbiology 144:793-800(1998).
CC -!- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
DR InterPro; IPR006662; Thiored.
DR InterPro; IPR006663; Thioredox_dom2.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KW Redox-active center; Electron transport.
FT DISULFID 29 32 REDOX-ACTIVE (BY SIMILARITY).
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4525 MW; C7BE3C913E3E2909 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 LVLD 37
 |||||
Db 2 LVLD 5

RESULT 31
UC11_MAIZE
ID UC11_MAIZE STANDARD; PRT; 40 AA.
AC P80617;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 207)
DE (Fragments).

OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.2, ITS MW IS: 27.1 kDa.
CC -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. HSP26 FAMILY.
CC -!- CAUTION: THE ORDER OF THE PEPTIDES SHOWN IS UNCERTAIN.
DR Maize-2DPAGE; P80617; COLEOPTILE.
DR MaizeDB; 123940; -.
FT NON_TER 1 1
FT NON_CONS 13 14
FT NON_CONS 26 27
FT NON_CONS 35 36
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4475 MW; 2ACD4BF8F4908277 CRC64;

Query Match 10.3%; Score 4; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLAA 19
||||
Db 18 LLAA 21

RESULT 32
CH60_MYCSM
ID CH60_MYCSM STANDARD; PRT; 28 AA.
AC P80673;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Fragment).
GN GROL OR GROEL OR MOPA.
OS Mycobacterium smegmatis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 607 / mc(2)6 / NRRL B-692;
RX MEDLINE=97387814; PubMed=9243799;
RA Lundrigan M.D., Arceneaux J.E.L., Zhu W., Byers B.R.;
RT "Enhanced hydrogen peroxide sensitivity and altered stress protein
RT expression in iron-starved Mycobacterium smegmatis.";
RL BioMetals 10:215-225(1997).
CC -!- FUNCTION: Prevents misfolding and promotes the refolding and

CC proper assembly of unfolded polypeptides generated under stress
CC conditions.
CC -!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
CC 7 subunits (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
DR HAMAP; MF_00600; -; 1.
DR InterPro; IPR001844; Chaprnnin_Cpn60.
DR PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.
KW Chaperone; ATP-binding.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3047 MW; 2F40F27B94EF8720 CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLA 3
|||
Db 20 SLA 22

RESULT 33
MAAI_RAT
ID MAAI_RAT STANDARD; PRT; 28 AA.
AC P57113;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Maleylacetoacetate isomerase (EC 5.2.1.2) (MAAI) (Glutathione S-
DE transferase zeta 1) (EC 2.5.1.18) (GSTZ1-1) (Fragment).
GN GSTZ1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=Fischer 344; TISSUE=Liver;
RX MEDLINE=98198370; PubMed=9531472;
RA Tong Z., Board P.G., Anders M.W.;
RT "Glutathione transferase zeta catalyses the oxygenation of the
RT carcinogen dichloroacetic acid to glyoxylic acid.";
RL Biochem. J. 331:371-374(1998).
CC -!- FUNCTION: PROBABLE BIFUNCTIONAL ENZYME SHOWING MINIMAL
CC GLUTATHIONE-CONJUGATING ACTIVITY WITH ETHACRYNIC ACID AND 7-
CC CHLORO-4-NITROBENZ-2-OXA-1, 3-DIAZOLE AND MALEYLACETOACETATE
CC ISOMERASE ACTIVITY. HAS ALSO LOW GLUTATHIONE PEROXIDASE ACTIVITY
CC WITH T-BUTYL AND CUMENE HYDROPEROXIDES (BY SIMILARITY). IS ABLE TO
CC CATALYZE THE GLUTATHIONE DEPENDENT OXYGENATION OF DICHLOROACETIC
CC ACID TO GLYOXYLIC ACID.
CC -!- CATALYTIC ACTIVITY: 4-maleylacetoacetate = 4-fumarylacetoacetate.
CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -!- COFACTOR: THE MAAI ACTIVITY REQUIRES GLUTATHIONE (BY SIMILARITY).
CC -!- PATHWAY: Phenylalanine catabolism; fifth step.
CC -!- PATHWAY: Tyrosine catabolism; fourth step.
CC -!- SUBUNIT: Homodimer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: THE N-TERMINUS IS BLOCKED (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. ZETA FAMILY.
KW Isomerase; Transferase; Multifunctional enzyme;
KW Phenylalanine catabolism; Tyrosine catabolism.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 2943 MW; 1070608C44491C25 CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ALE 21
|||
Db 11 ALE 13

RESULT 34
OBP1_HYSCR
ID OBP1_HYSCR STANDARD PRT; 28 AA.
AC P81647;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Odorant-binding protein I (OBP I) (Olfactory mucosa pyrazine-binding protein I) (Fragment).
OS Hystrix cristata (Crested porcupine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Hystricidae; Hystrix.
OX NCBI_TaxID=10137;
RN [1]
RP SEQUENCE.
RC TISSUE=Nasal mucosa;
RX MEDLINE=97370581; PubMed=9226887;
RA Ganni M., Garibotti M., Scaloni A., Pucci P., Pelosi P.;
RT "Microheterogeneity of odorant-binding proteins in the porcupine revealed by N-terminal sequencing and mass spectrometry.";
RL Comp. Biochem. Physiol. 117B:287-291(1997).
RN [2]
RP CHARACTERIZATION.
RC TISSUE=Nasal mucosa;
RX MEDLINE=93373535; PubMed=8365121;
RA Felicioli A., Ganni M., Garibotti M., Pelosi P.;
RT "Multiple types and forms of odorant-binding proteins in the Old-World porcupine *Hystrix cristata*.";
RL Comp. Biochem. Physiol. 105B:775-784(1993).
CC -!- FUNCTION: This soluble protein may play a specific role in odor discrimination and perception.
CC -!- SUBCELLULAR LOCATION: Secreted; Extracellular.
CC -!- TISSUE SPECIFICITY: Nasal mucosa.
CC -!- SIMILARITY: Belongs to the lipocalin family.
DR HSSP; Q95182; 1EW3.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR PROSITE; PS00213; LIPOCALIN; 1.
KW Olfaction; Transport; Lipocalin.
FT NON_TER 28 28

SQ SEQUENCE 28 AA; 3240 MW; D12E8CAC87E38AB3 CRC64;
Query Match 7.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLA 18
|||
Db 21 LLA 23

RESULT 35
ORND_PLAOR
ID ORND_PLAOR STANDARD; PRT; 28 AA.
AC P25513;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ornatin D (Fragment).
OS Placobdella ornata (Turtle leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Placobdella.
OX NCBI_TaxID=6415;
RN [1]
RP SEQUENCE.
RX MEDLINE=92111479; PubMed=1765068;
RA Mazur P., Henzel W.J., Seymour J.L., Lazarus R.A.;
RT "Ornatin: potent glycoprotein IIb-IIIa antagonists and platelet
RT aggregation inhibitors from the leech Placobdella ornata.";
RL Eur. J. Biochem. 202:1073-1082(1991).
CC -!- FUNCTION: POTENT INHIBITOR OF FIBRINOGEN INTERACTION WITH PLATELET
CC RECEPTORS EXPRESSED ON GLYCOPROTEIN IIb-IIIa COMPLEX. MAY PREVENT
CC BLOOD FROM CLOTTING DURING EITHER FEEDING AND/OR STORAGE OF
CC INGESTED BLOOD.
CC -!- SIMILARITY: BELONGS TO THE ORNATIN FAMILY.
DR InterPro; IPR002463; Ornatin.
DR Pfam; PF02088; Ornatin; 1.
KW Blood coagulation; Platelet; Cell adhesion.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3361 MW; CFC38951F91337C2 CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 FRE 12
|||
Db 16 FRE 18

RESULT 36
SMS2_ORENI
ID SMS2_ORENI STANDARD; PRT; 28 AA.
AC P81029;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Somatostatin II precursor [Contains: [Tyr21,Gly24]somatostatin-28;
DE [Tyr7,Gly10]somatostatin-14] (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE.
RX MEDLINE=95384941; PubMed=7656183;
RA Nguyen T.M., Wright J.R. Jr., Nielsen P.F., Conlon J.M.;
RT "Characterization of the pancreatic hormones from the Brockmann body
of the tilapia: implications for islet xenograft studies.";
RL Comp. Biochem. Physiol. 111C:33-44(1995).
CC -!- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
DR InterPro; IPR004250; Somatostatin.
DR Pfam; PF03002; Somatostatin; 1.
KW Cleavage on pair of basic residues; Hormone; Multigene family.
FT NON_TER 1 1
FT PEPTIDE 1 28 [TYR21,GLY24] SOMATOSTATIN-28.
FT PEPTIDE 15 28 [TYR7,GLY10] SOMATOSTATIN-14.
FT DISULFID 17 28
SQ SEQUENCE 28 AA; 3155 MW; 47C049F4866EF4AC CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RER 13
|||
Db 11 RER 13

RESULT 37
VIP_ALLMI
ID VIP_ALLMI STANDARD; PRT; 28 AA.
AC P48142; P01285;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Vasoactive intestinal peptide (VIP).
GN VIP.
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=93324451; PubMed=8101369;
RA Wang Y., Conlon J.M.;
RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
and stomach of the alligator.";
RL Peptides 14:573-579(1993).

CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
CC AND GALL BLADDER.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Amidation; Hormone.
FT MOD_RES 28 28 AMIDATION.
SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 LNS 28
|||
Db 23 LNS 25

RESULT 38
VIP_DIDMA
ID VIP_DIDMA STANDARD; PRT; 28 AA.
AC P39089;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vasoactive intestinal peptide (VIP).
GN VIP.
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267;
RN [1]
RP SEQUENCE.
RX MEDLINE=92179271; PubMed=1542675;
RA Eng J., Yu J.-H., Rattan S., Yalow R.S.;
RT "Isolation and amino acid sequences of opossum vasoactive intestinal
RT polypeptide and cholecystokinin octapeptide.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:1809-1811(1992).
CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
CC AND GALL BLADDER.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; A38232; A38232.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Amidation; Hormone.
FT MOD_RES 28 28 AMIDATION.
SQ SEQUENCE 28 AA; 3318 MW; F01188A0A72F76D9 CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 RLL 17
|||
Db 12 RLL 14

RESULT 39

VIP_RANRI
ID VIP_RANRI STANDARD; PRT; 28 AA.
AC P81016;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Vasoactive intestinal peptide (VIP).
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RX MEDLINE=95309202; PubMed=7540547;
RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
RT "Frog vasoactive intestinal polypeptide and galanin: primary
structures and effects on pituitary adenylate cyclase.";
RL Endocrinology 136:3079-3086(1995).
CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
CC AND GALL BLADDER.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Amidation; Hormone.
FT MOD_RES 28 28 AMIDATION.
SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 LNS 28
|||
Db 23 LNS 25

RESULT 40

VIP_SCYCA
ID VIP_SCYCA STANDARD; PRT; 28 AA.
AC P09685;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Vasoactive intestinal peptide (VIP).
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RX MEDLINE=87299819; PubMed=2441759;
RA Dimaline R., Young J., Thwaites D.T., Lee C.M., Shuttleworth T.J.,
RA Thorndyke M.C.;
RT "A novel vasoactive intestinal peptide (VIP) from elasmobranch
RT intestine has full affinity for mammalian pancreatic VIP receptors.";
RL Biochim. Biophys. Acta 930:97-100(1987).
RN [2]
RP SEQUENCE.
RA Dimaline R., Young J., Thwaites D.T., Lee C.M., Thorndyke M.C.;
RT "Amino acid sequence of a biologically active vasoactive intestinal
RT peptide from the elasmobranch Scyliorhinus canicula.";
RL Ann. N.Y. Acad. Sci. 527:621-623(1988).
RN [3]
RP SEQUENCE OF 1-10.
RX MEDLINE=86234323; PubMed=3715063;
RA Dimaline R., Thorndyke M.C., Young J.;
RT "Isolation and partial sequence of elasmobranch VIP.";
RL Regul. Pept. 14:1-10(1986).
CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
CC AND GALL BLADDER.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; A60303; A60303.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Amidation; Hormone.
FT MOD_RES 28 28 AMIDATION.
SQ SEQUENCE 28 AA; 3270 MW; 9014389573F81F3B CRC64;

Query Match 7.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLA 18
|||
Db 26 LLA 28

Search completed: January 14, 2004, 10:35:42
Job time : 8.43925 secs